

PATENT APPLICATION

TAG NUCLEIC ACIDS AND PROBE ARRAYS

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TAG NUCLEIC ACIDS AND PROBE ARRAYS

PRIORITY CLAIM

This application claims priority of U.S. Provisional Application 60/195,585 filed April 6, 2000 entitled "Tag Nucleic Acids and Probe Arrays", which is incorporated herein by reference for all purposes in its entirety.

FIELD OF THE INVENTION

This invention provides sets of nucleic acid tags, arrays of oligonucleotide probes, nucleic acid-tagged sets of recombinant cells and other compositions. The invention relates to the selection and interaction of nucleic acids, and nucleic acids immobilized to solid substrates, including related chemistry, biology, and medical diagnostic uses.

BACKGROUND OF THE INVENTION

The use of short nucleic acid sequences as "tags" to identify specific biological substances in a sample is known. For example, tags may be used as a method of or as labels for a wide variety of biological and nonbiological materials, see, for example, Dollinger, The Polymerase Chain Reaction pp. 265-274 Mullis et al., editors (Birkhauser, Boston, 1994) or as a method of screening complex chemical libraries. See, for example, Alper, Science, 264: 1399-1401 (1994); and Needels et al. PNAS 90, 10700-10704 (1993). See also US Patent Nos. 4,359,353, 4,441,943, 5,451,505 and 5,654,413.

There is great necessity for sets of tag sequences which are known to hybridize effectively to their complementary probe sequences with minimal cross-hybridization between the different tag sequences. The presently claimed invention provides sets of tag sequences, tag sequence kits, and methods of using tag sequences which fulfill these requirements.

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SUMMARY OF THE INVENTION

The presently claimed invention provides 2050 unique sequences which have been specifically chosen according to strict criteria to produce sequences suitable for a wide variety of "tagging" applications. These sequences are provided as SEQ ID NOs 1-2050.

In one embodiment, some or all of SEQ ID Nos 1-2050 comprise tag sequences. In a further embodiment, some or all of SEQ ID Nos 1-2050 comprise tag-probe sequences. In a further embodiment, the tag-probe sequences are immobilized to a solid support.

The unique sequences of the presently claimed invention may be used alone or in combinations of 10 or more, 100 or more, 200 or more, 500 or more, 1000 or more, 1500 or more, or 2000 or more as nucleic acid tags and/or tag-probes.

BRIEF DESCRIPTION OF THE DRAWINGS

- FIG. 1 shows a plot of the discrimination score and the signal intensity for 2200 candidate sequences.
- FIG. 2 shows an example of the sequences attached to each of the four array features representing a given tag sequence. Four features, organized vertically on the probe array, represent each tag-probe.
- FIG. 3 shows the array features from an array designed to probe for the tag sequences of the presently claimed invention. For each of the four tag-probes shown, arranged horizontally across the array, the brightest hybridization signal is seen with the "PM" feature.
- FIG. 4 is a scanned image of the hybridization patterns resulting from the hybridization of 2050 different probes containing regions complementary to the SEQ ID Nos 1-2050 to an array comprised of tag-probes corresponding to SEQ ID Nos 1-2050.
- FIG.5 is a scanned image of the hybridization patterns resulting from the hybridization of 50 different probes containing regions complementary to SEQ ID Nos 2001-2050 to an array identical to the array depicted in FIG. 4.

FIG. 6 shows signal intensities from two different independent experiments in which 2000 biotinylated oligonucleotide tags or 50 fluorescein labeled control oligonucleotides were hybridized to arrays designed as described above.

FIG. 7 shows the PM/MM ratios from the data described in FIG. 4 above.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

I. Definitions

As used herein, certain terms may have the following defined meanings.

As used in the specification and claims, the singular forms "a", "an" and "the" include plural references unless the context clearly dictates otherwise. For example, the term "an array" may include a plurality of arrays unless the context clearly dictates otherwise.

An "array" represents an intentionally created collection of molecules which can be prepared either synthetically or biosynthetically. In particular, the term "array" herein means an intentionally created collection of polynucleotides attached to at least a first surface of at least one solid support wherein the identity of each polynucleotide at a given predefined region is known. The terms "array," "biological chip" and "chip" are used interchangeably.

The array of molecules can be screened for biological activity in a variety of different formats (*e.g.*, libraries of soluble molecules, libraries of compounds tethered to resin beads, fibers, silica chips, or other solid supports). The fabrication of polynucleotide arrays on a solid substrate, and methods of use of the arrays in different assays, are described in US Patent Numbers: 5,143,854, 5,242,979, 5,252,743, 5,324,663, 5,384, 261, 5,405,783, 5,412,087, 5,424,186, 5,445,934, 5,451,683, 5,482,867, 5,489,678, 5,491,074, 5,510,270, 5,527,681, 5,550,215, 5,571,639, 5,593,839, 5,599,695, 5,624,711, 5,631,734, 5,677,195, 5,744,101, 5,744,305, 5,744,992, 5,753,788, 5,770,456, 5,831,070, 5,856,011, 6,040,138 and 6,040,193 all of which are incorporated by reference herein in their entireties for all purposes. See also, US Serial Nos. 09/079,324, 09/122,216, and PCT Application WO US99/00730 each of which is incorporated by reference herein in its entirety for all purposes. Preferred arrays contemplated by the presently claimed invention have the probe densities as described in the above referenced patents. For example, the '305 patent discloses 100, 400, 1,000 and 10,000 probes/cm².

"Solid support," "support," and "substrate" refer to a material or group of materials having a rigid or semi-rigid surface or surfaces. In many embodiments, at least one surface of the solid support will be substantially flat, although in some embodiments it may be desirable to physically separate synthesis regions for different compounds with, for example, wells, raised regions, pins, etched trenches, or the like. According to other embodiments, the solid support(s) will take the form of beads, resins, gels, microspheres, fibers or other geometric configurations.

A "discrete, known location" refers to a localized area on a solid support which is, was, or is intended to be used for placement or fabrication of a selected molecule and is otherwise referred to herein in the alternative as a "selected" region. The discrete, known location may have any convenient shape, e.g., circular, rectangular, elliptical, wedge-shaped, etc. For the sake of brevity herein, "discrete, known locations" are sometimes referred to as "predefined regions," "regions," or "features." In some embodiments, a discrete, known location and, therefore, the area upon which each distinct compound is synthesized is smaller than about 1 cm² or even less than 1 mm². In additional embodiments, a discrete, known location can be achieved by physically separating the regions (i.e., beads, fibers, resins, gels, etc.) into wells, trays, etc.

As used herein, a "polynucleotide" is a sequence of two or more nucleotides. Polynucleotides of the present invention include sequences of deoxyribonucleic acid (DNA) or ribonucleic acid (RNA) which may be isolated from natural sources, recombinantly produced, or artificially synthesized. A further example of a polynucleotide of the present invention may be polyamide polynucleotide or peptide nucleic acid (PNA). This invention also encompasses situations in which there is nontraditional base pairing such as Hoogsteen base pairing which has been identified in certain tRNA molecules and postulated to exist in a triple helix. "Polynucleotide" is used interchangeably with "oligonucleotide" is this application.

The terms "nucleotide" and "nucleic acid base" include deoxynucleotides and analogs thereof. These analogs are those molecules having some structural features in common with a naturally occurring nucleotide such that when incorporated into a polynucleotide sequence, they allow hybridization with a complementary polynucleotide in solution. Typically, these analogs may have one or more modified bases, as well as modified forms of ribose and phosphodiester moieties. The changes can be tailor made to stabilize or destabilize hybrid formation, enhance

the specificity of hybridization with a complementary polynucleotide sequence as desired, or enhance stability of the polynucleotide.

The terms "nucleic acid," "nucleic acid molecule," or "nucleic acid sequence," refer to a deoxyribonucleotide or ribonucleotide polymer in either single-or double-stranded form, and unless otherwise limited, would encompass analogs of natural nucleotides that can function in a similar manner as naturally occurring nucleotides. Nucleic acids may be derived from a variety or sources including, but not limited to, naturally occurring nucleic acids, clones, synthesis in solution or solid phase synthesis.

As used herein a "probe" is defined as a nucleic acid capable of binding to a target nucleic acid of complementary sequence through one or more types of chemical bonds, usually through complementary base pairing, usually through hydrogen bond formation. As used herein, a probe may include natural (i.e. A, G, U, C, or T) or modified bases (7-deazaguanosine, inosine, etc.). In addition, the bases in probes may be joined by a linkage other than a phosphodiester bond, so long as it does not interfere with hybridization. Thus, probes may be peptide nucleic acids in which the constituent bases are joined by peptide bonds rather than phosphodiester linkages.

The term "target nucleic acid" or "target sequence" refers to a nucleic acid or nucleic acid sequence which is to be analyzed. A target can be a nucleic acid to which a probe will hybridize. The probe may or may not be specifically designed to hybridize to the target. It is either the presence or absence of the target nucleic acid that is to be detected, or the amount of the target nucleic acid that is to be quantified. The term target nucleic acid may refer to the specific subsequence of a larger nucleic acid to which the probe is directed or to the overall sequence (e.g., gene or mRNA) whose expression level it is desired to detect. The difference in usage will be apparent from context.

The term "hybridization" refers to the process in which two single-stranded polynucleotides bind non-covalently to form a stable double-stranded polynucleotide; triple-stranded hybridization is also theoretically possible. The resulting (usually) double-stranded polynucleotide is a "hybrid." The proportion of the population of polynucleotides that forms stable hybrids is referred to herein as the "degree of hybridization." Hybrids can contain two DNA strands, two RNA strands, or one DNA and one RNA strands.

Methods for conducting polynucleotide hybridization assays have been well developed in the art. Hybridization assay procedures and conditions will vary depending on the application and are selected in accordance with the general binding methods known including those referred to in: Molecular Cloning, A Laboratory Manual, Second Ed., J. Sambrook et al., Eds., Cold Spring Harbor Laboratory Press, 1989 ("Sambrook et al."); Berger and Kimmel, "Methods in Enzymology," Vol. 152, "Guide to Molecular Cloning Techniques", Academic Press, Inc., San Diego, CA., 1987; Young and Davis, *Proc. Natl. Acad. Sci.*, U.S.A., <u>80</u>:1194 (1983), each of which are incorporated herein by reference.

It is appreciated that the ability of two single stranded polynucleotides to hybridize will depend upon factors such as their degree of complementarity as well as the stringency of the hybridization reaction conditions.

As used herein, "stringency" refers to the conditions of a hybridization reaction that influence the degree to which polynucleotides hybridize. Stringent conditions can be selected that allow polynucleotide duplexes to be distinguished based on their degree of mismatch. High stringency is correlated with a lower probability for the formation of a duplex containing mismatched bases. Thus, the higher the stringency, the greater the probability that two single-stranded polynucleotides, capable of forming a mismatched duplex, will remain single-stranded. Conversely, at lower stringency, the probability of formation of a mismatched duplex is increased.

A nucleic acid "tag" is a selected nucleic acid with a specified nucleic acid sequence. A nucleic acid "probe" hybridizes to a nucleic acid "tag."

A nucleic acid "tag-probe" is a specific sequence capable of hybridizing to a specific "tag." Typically, the "tag-probe" is the complement or a partial complement of the "tag." In one typical configuration, nucleic acid tags are incorporated as labels into biological libraries, and the tag nucleic acids are detected using a microarray.

Throughout this disclosure, various aspects of this invention are presented in a range format. It should be understood that the description in range format is merely for convenience and brevity and should not be construed as an inflexible limitation on the scope of the invention.

Accordingly, the description of a range should be considered to have specifically disclosed all the possible sub-ranges as well as individual numerical values within that range. For example, the description of a range such as 4 to 50 should be considered to have specifically disclosed all integers within the sub-ranges such as 4 to 10, 4 to 20, 4 to 30, 4 to 40, 4 to 50, 5 to 10, 5 to 20 etc., as well as individual numbers within that range, for example, 6, 8, 15, 20, 32, 39, 43, 48 etc. This applies regardless of the breadth of the range. Likewise, a description of a range such as 1 or more, 10 or more, 10^3 or more, 10^6 or more, or 10^{12} or more should be considered to have specifically disclosed individual numbers within that range as well as higher numbers, for example, 20, $2x10^4$, $3x10^8$, $4x10^{15}$, $5x10^{18}$, etc.

Various patents, patent applications and publications are referenced throughout the specification, unless otherwise indicated, each is incorporated by reference in its entirety for all purposes.

II. General

The presently claimed invention provides 2050 unique sequences which have been specifically chosen according to strict criteria to produce sequences suitable for a wide variety of "tagging" applications. These sequences are provided as SEQ ID NOs 1-2050.

In one embodiment, some or all of SEQ ID Nos 1-2050 comprise tag sequences. In a further embodiment, some or all of SEQ ID Nos 1-2050 comprise tag-probe sequences. In a further embodiment, the tag-probe sequences are immobilized to a solid support.

An initial set of 2200 20mer sequences was selected with closely matched melting temperatures. A further filter based on rules such as those described in US Provisional Patent Application 60/176,520 was applied to optimized and standardize the hybridization characteristics of the set. Finally, sequences were removed if they were identical or nearly identical to each other or to sequences in the public databases. This reduced the pool of candidate sequences to 2200. The hybridization performance of the entire set of 2200 candidate sequences was evaluated. Labeled oligonucleotides complementary to the candidate sequences were synthesized and hybridized to an array containing probes designed to analyze the performance of all 2200 candidate sequences. The array contained four different sequences to

interrogate each candidate sequence. A probe designed to be the perfect match complement to the candidate sequence (PM), a probe designed to have a central mismatch at position 10 (MM), and probes designed to be the complements to the PM and MM probes (cPM and cMM respectively).

FIG. 1 shows a plot of the discrimination score and the signal intensity for all 2200 sequences. A line was fitted to select the 2050 sequences with the highest discrimination and signal intensity. These 2050 sequences are SEQ ID Nos. 1-2050.

In one embodiment of the invention, the sequences of the presently claimed invention are tag-probes attached to a solid support. Methods of immobilizing presynthesized sequences and synthesizing sequences de novo on solid supports are known. See for example, US Patent Numbers: 5,143,854, 5,242,979, 5,252,743, 5,324,663, 5,384, 261, 5,405,783, 5,412,087, 5,424,186, 5,445,934, 5,451,683, 5,482,867, 5,489,678, 5,491,074, 5,510,270, 5,527,681, 5,550,215, 5,571,639, 5,593,839, 5,599,695, 5,624,711, 5,631,734, 5,677,195, 5,744,101, 5,744,305, 5,753,788, 5,770,456, 5,831,070, 5,856,011, 5,744,992, 6,040,138, 6,040,193, US Serial Nos. 09/079,324, 09/122,216, and PCT Application WO US99/00730.

In this and other embodiments it is often useful to provide control probes. As one example, SEQ ID Nos. 1-2000 may comprise the tag-probes and SEQ ID Nos. 2001-2050 may comprise the control probes. In a preferred embodiment, the control probes are representative of the population with respect to observed signal intensities and discrimination. In a further preferred embodiment, tag sequences with relatively low signals may be over-represented in the control sequences so as to increase information about the sensitivity of experiments at the lower limit of detection.

METHODS OF USE

The use of short nucleic acid sequences as "tags" to identify specific biological substances in a sample is known. For example, tags may be used as a method of or as labels for a wide variety of biological and nonbiological materials, see, for example, Dollinger, The Polymerase Chain Reaction pp. 265-274 Mullis et al., editors (Birkhauser, Boston, 1994) or as a method of screening complex chemical libraries. See, for example, Brenner and Lerner, PNAS

89, 5281-5383 (1992); Alper, Science, 264: 1399-1401 (1994); and Needels et al. PNAS 90, 10700-10704 (1993). See also US Patent Nos. 4,359,353, 4,441,943, 5,451,505 5,149,625, 5,654,413 and 5,800,992.

In addition to those applications above, the presently claimed sequences are suitable to be employed for any of the methods described in US Patent Application No. 08/626,285 (filed 4/4/96), including as a method of analysis of genomic DNA. For example, as described in the '285 application, tag arrays may be used to identify the function of identified open reading frames (ORFs) by creating deletion mutants for each ORF and analyzing the resulting deletion mutants under a wide variety of selective conditions.

US Provisional Patent Application No. 60/140,359 (filed 6/23/99) described methods of using tag arrays and the single base extension reaction for genotyping and other types of biological analysis. A set of tags and a tag array derived from Seq. ID Nos. 1-2000 and their complements are suitable to be used for the methods described in this application. Briefly, the '359 application describes methods of determining the genotype of an individual at a polymorphic locus or the frequency of alleles in a population. One embodiment of the method involves three step: (1) amplification of the polymorphic locus, (2) primer extension of a sequence-tagged primer with distinct labels for different polynucleotides at the polymorphic locus, and (3) hybridization to a tag array. The amount of each distinct label can be determined at known positions of the tag array. Each tag represents a distinct polymorphic locus and each distinct label represents a distinct allelic form at the polymorphic locus. The method permits the simultaneous determination of a genotype at multiple loci, as well as the determination of allele frequencies in a population. Another embodiment employs just steps (2) and (3).

Table 1, below, lists the sequences of the presently claimed invention. Column 1 lists the sequence ID number corresponding to each sequence. Column 2 lists the sequences in the 3' to 5' direction.

TABLE I

Seq. Id	3' to 5' sequence	
1	TAAACTAGCATTGAGCCCAC	
2	AAATCAGCAAACGGGCTCCG	
3	GAATTGATAATCGCAGCCAC	
4	GATATAGGAATGGCGCATAC	

Con Id	O'to E' coguence
Seq. Id	3' to 5' sequence
5	CTCATCGGAAGGGCTCGTAA
5 6 7	ACAGATGGAAAGGCAGTTCT
	TTTGGTAGCTGAGTGCCCTA
8	TAACTGGTTTGACGCCACGC
9	TAATTGAGCTGACGGCGCAC
10	TTGTTGCTACTCTGGCCCGA
11	TTCCGTGCATAGTATAGGGA
12	TTATGCGACTTATCTCGGGA
13	TGTATAGGATTATGTCCGCG
14	CTGCTAGGAATATGAGCTAC
15	CTTCTGTCAATATGGGTACG
16	TATTTCGAGATATGAGGCGC
17	TTGATCGTAGATTCGTGAGC
18	CGAGATTACAATTCACGAGC
19	TGGTGTCTAGCTTCCAGCCT
20	TGAGGTCACGGTTCATGCTA
21	TGGTTACTGGTATATGCCGC
22	CCGAGTGCAGAATAAACCCG
23	GCGGTCTCAATACAAACTCA
24	GAAGCTACCATACGCGAGCA
25	ACGGGATAACAACGCAGCCT
26	AGAAGATCAACAGCTCGTCC
27	ATAAGATCAAGACCTGTGCC
28	ATTAGATTAAGACCAGCGCC
29	ATATAATCAAGACTGGCGCG
30	AGCATATAACCACTGATCCG
31	ACACTATTAAAGCTGCTCCG
32	CAATGTATAAGACTCTCGCC
33	CACTAATTCAGACGAAGCCG
34	GACCCTATCAGACAGATGCA
35	CACGCATCAAGACAGTATCG
36	CAGCTCCTAAGACTTGGACA
37	GGTATCATAGGACATTCGCA
38	GGTTACATGGATATAGCACC
39	TGTGTTTCAGCTATGCAGGC
40	TAATTCGCTGCAACCAGATC
41	ATAATTCCAACATGGGAGCC
42	CATTGCTTAATATGGGAGCC
43	CAATGCTTAATACCGACACG
44	GATTGCTTAGACCCTGCACG
45	GATTCATTAGACCAGGCGCT
46	GATTCTACATGCCACTAGCA
47	CCTGCGAACTGCCACTAGCA
48	
) 	CGCAGCGGAAGGCTCAATAA CCTACCGCAAGGCAGGATAA
49	
50	CCTATGATAAGGCACGCACA
51	CGCTGTGCAAGGCTCGTATA
52	CGATTGTCAAGGCAGTGATA

CATTGCGAACTGCATCTAAC GATAGTCCAATGCTACTGAC GATAGTCCAATGCTACTGAC GATTCGGTAATGCGCTGTAA GACGTTTCAATGCAGCGTAA GACGTTCCAATGCAACGCGTAA GACGATCCAATGCCGACTAA GACGATCCAATGCCGCACTAA GACGATCCAAGGCCCATGAT GAGAGTCCAAGGCCCATGAT GACGATCCAAGGCCCATGAT GACGATCCAAGGCCCATGAT GACGATCCAAGGCCCATGAT GACGATCCAAGGCCCATGAT GACGATCCAAGGCCCATGAT GACGATCCAAGGCCCATGAT GACGATCCAAGGCCCATGAT GACGATTGCACCATGACCCT GACGATCACCCCTCAG GACTTGCACAGTACCCT GACGATATTGGATACCCCC GACGATATTGGATACCCCC GATTGCAGAATGGCGTGATCC GACGAATAAGGCCACGATA GACCCCCCCCCC	Seq. Id	3' to 5' sequence
GATAGTCCAATGCTACTGAC GATTCGGTAATGCGCTGTAA GAGAGTGCAATGCGCGTAA GAGAGTCCAATGCCGACTAA GAGAGTCCAAGGCCACTAA GAGAGTCCAAGGCCCACTAA GAGAGTCCAAGGCCCATGAT GAGAGTCCAAGGCCCATGAT GAGAGTCCAAGGCCCATGAT GAGAGTCCAAGGCCCATGAT GAGAGTTGAACAGCATACCCT GAGAGTTGAACAGGCCATGAT GAGAGTTGAACAGCATACCCT GAGAGTTGAACAGCATACCCT GAGAGTTGAACAGCATACCCT GAGAGTTGAACAGCATACCCT GATTGGACTATTGGGTATCGCC GATTGCAGATTGGATCGCCC GATTGCAGATTGGATCGCCC GATTGCAGATTGGATCGCCC GATTGCAGATTAGGCACTCAGC CATTGGATAAGCACTGATCC GAGAGCAAATAGGCCACATA GAGAGCAAATGACACCCCACC CATAGATTAAGCACTCAGCC CATAGATTAAGCACTCACCC CAGAGACGAAGACACTCACCC CAGAGCGAAGAGCACTCACC TACATAGGCTTCAGCATCAC TACATAGGCTTCAGCATCAC TACATAGCCTTGATCCGCCC TAAACTGCTTGCATACCGCC TAAACTGCTTGCAACCGCACC TAAACTGCTTGCAACCGCACC TAAACTGCTTGCAACCGCACC TAAACTGCTTGCAACCGCCC TAAACTGCTTGCAACCGCCC TAAACTGCTTGCAACCGCCC TAAACTGCTTGCAACCGCCC TAAACTGCTTGCAACCGCCC TAAACTGCTTGCAACCGCCC TAAACTGCTTGCAACCGCCC TAAACTGCTTGCAACCGCCCC TAAACTGCTTGCAACCGCCC TAAACTGCTTGCAACCGCCC TAAACTGCTTGCAACCGCCC TAAACTCTTGCAACCCCCCC TAAACTCTTGAACCCCCCCC TAAAACTCTTGAACCCCCCCCCC		<u> </u>
55 GATTCGGTAATGCGCTGTAA 56 GACGTTTCAATGCAGCGTAA 57 GAGAGTGCAATGCCGACTAA 58 GAGATCCGAATGCCGACTAA 58 GAGATCCGAATGCCGACTA 59 CGAGATCCAAGGCCCATGAT 60 AGCTTGCACAGTAACCATGA 61 AGAGTTGAACAGCATACCCT 62 TATCTGATCGGACGGCCAGT 63 TATTGACTACTGCGCCTCAG 64 TTGGACTATTGGGTATCGCC 65 TTGTCAGATTGGATGCGCTC 66 TATGCAGATAGCACTGATC 67 CATTGGATAGCACTGATC 68 CCCGGAATAAGCACTGATC 69 CTCATAGAATGGACCAGATA 69 CTCATAGAATGAGCACTGATC 70 CATAGATTAAGCACTCAGC 71 CATGATGTAAGCACTCAGC 72 CAGGAGCGAAGACACCCTACC 72 CAGGAGCGAAGACACTCACC 73 CAGAGCAGAAGCACTCACC 74 TACATAGGCTTCAGCATCAC 75 TATTATACCTTGATCCGCG 76 TAAACTGCTTGCATCACGC 77 TATAAGCCTTGCATCACC 78 TTTAAGCGTTGCATCACC 79 TTAAACCGTTGCAGCAC 80 ATAAATGCTTGGAACCCTCG 81 GAAAGTTCATGGAACCCTCG 82 GCAAGGATTCTGGAACCCTCG 83 CAAAGAATAATCGCTCCCG 84 TAAACTGCTTGACACCCCC 85 TTATATACCTTGATCCGCC 86 TAAACTGCTTGAGCAGCA 87 CAAACTGCTTGAACCCTCG 88 ATAAATGCTTGGAACCCTCG 89 ACAAGAATTAATCGCTCCTCG 80 ATAAATTCGTCAGCAC 81 GAAAGTTCATGAACCCCCC 82 GCAAGGATTTCGACTCAGAC 83 CAAAGAATAATCGCTCCTCG 84 TAAAGCACTTATGACTCAGCC 85 TTATAGCACTTAGACTCAGC 86 TCCCTGACATTTGATTAGCC 87 CCTTGAATAATATCGCCC 88 AGGTCCAGAAATTATGCCC 89 AGCTCAGGAAATTCTAGCAC 90 AGCTATGCAAATTAATACCCT 91 GGTAGGCTAATTTATGGCAC 92 CTAATGCAATTCAATGCCC 93 CAACTGCAAATTAATACGCT 94 CCAAGCGAAATTCAATACGCT 95 GCACAGCAATTCAATACGCT 96 GCATGCCAATCAATACGCT 97 GCACGTTCAATGGATAC 97 GCACGTTCAATTGGATAC 97 GCACGTTCAATTGGATAC 98 GCAGCGCAATCAATACGCT 99 GCACGTTCAATTGGATAC 99 GCACGTTCAATTGGATAC 99 GCACGTTCAATTGGATAC 99 GCACGTTCAATTGGATAC 99 GCACGTTCAATTGGATAC 99 GCACGTTCAATTGGATAC		
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TACATAGGCTTCAGCATCAC TACATAGGCTTCAGCATCAC TACATAGGCTTCAGCATCAC TACATAGGCTTGATCCGCGC TACACTGCTTGCATCGGCG TACACTGCTTGCATCGGCG TACACTGCTTGCAGCGGACC TACACTGCTTGCAGCGGACC TACACTGCTTGCAGCGGACC TACACTGCTTGAGCAGCGA TACACTGGAACCCTCG TACACTGGAACCCTCG TACACTGGAATCGACC TACACTGGAATCGACC TACACTGGAATCGACC TACACTTCTGAGCTCCTCG TACACTTCTGTAGCCC TACACTTCTGTAGCCC TACACTTCTGACTCGGC TACACTTTGATTAGCC TACACTTCTGACTCGCC TACACTTCTGACTCGCC TACACTTCTGACTCGCC TACACTTCTGACTCGCC TACACTTCTGACTCGCC TACACTTCTGACTCGCC TACACTTCTGACTCGCC TACACTTCTGACCCC TACACTGCAAATTCTAGCGA TACACTGCAAATTCTAGCGC TACACTGCAAATTCAATGCCCC TACACTGCAATTCAATCCCCC TACACTGCAATTCAATCCCCC TACACTGCAATCCAATC	<u> </u>	· · · · · · · · · · · · · · · · · · ·
TACATAGGCTTCAGCATCAC TATTATACCTTGATCCGCGC TATTATACCTTGATCCGCGC TATTATACCTTGATCCGCGC TATTATACCTTGCATCCGCGC TATTATAGCCTTGCAGCGGACC TATTAAGCCTTGCAGCGGACC TATTAAGCCTTGAGCAGCGA TTTAATAGCCTTGAGCAGCGA ATAAATGCTTGGAACCCTCG B1 GAAAGTTCATGGAATCGAGC B2 GCAAGGATTTCGACTCAGAC B3 CAAAGAATAATCGCTCCTCG B4 TAAAGCACTTATGACTCGGC B5 TTATAGCATTCTGTAGGCGC B6 TCGCTGACATTTGATTAGCC B7 CCTTGAATAATATCTCGGCC B8 AGGTCCAGAAATTCTAGCGA B9 AGCTCAGGAAATTCTAGCGA B9 AGCTCAGGAAATTCTAGCGA B9 AGCTCAGGAAATTCAATGCCGC B1 GGTAGGCTAATTTATGCAC B2 CTAATGCAATTCAATGCCGC B3 CAACTGCAATTCAATGCCGC B4 CCAAGCGAATCAATACGCT B5 GCATGCGAATCAATACGCT B6 GCATGTCGAATGGATAC B7 GCACGTTCAATGGCTCGACT B8 GCACGCCAATCTGTCGACT B8 GCACGCCAATCTGTCGACT B8 GCACGCCAATCTGTCGACT B8 GCACGCCCAATCTGTCGACT B8 GCACGCCCAATCTGTCGACT B8 GCACGTGCAAATCCTGATAC		
TATTATACCTTGATCCGCGC TAAACTGCTTGCATACGGCG TAAACTGCTTGCATACGGCG TAAACTGCTTGCATCGGCG TAAACTGCTTGCAGCGGACC TATTAAGCCTTGCAGCGGACC TAATAGCCTTGAGCAGCGA TTAATAGCCTTGAGCAGCGA ATAAATGCTTGGAACCCTCG ATAAATGCTTGGAATCGAGC ACAAGGATTTCGACTCAGAC ACAAGGATTCGACTCCTCG ACAAGGATTCTGTAGGCGC ACAAGCACTTATGACTCGGC ACCTTGAATAATATCTCGGCC ACCTTGAATAATATCTCGGCC ACCTTGAATAATATCTCGGCC ACCTTGAATAATTTAGCCC ACCTTGAATATTTATGCCC ACCTTGAATATTTATGCCC ACCTTGAATATTTATGCCC ACCTTGAATATTTATGCCC ACCTTGCAATTTATGCCC ACCTTGCAATTTATGCCC ACCTTGCAATTTATGCCCC ACCTTGCAATTCAATGCCCC ACCTTGCAATTCAATGCCCC ACCTTGCAATTCAATGCCCC ACCTTGCAATTCAATGCCCC ACCTTGCAATTCAATGCCCC ACCTTCGAATGCAATTCAATCCCCC ACCTTCGAATGCAATTCCCCC ACCTTCGAATGGAGATAC ACCAGCGAATTCGAATCCCCC ACCAGCGAATTCGAATCCCCC ACCAGCGCAATCTGCCGACT ACCAGCGCCAATCTGCCGACT ACCAGCGCCAATCTGCCGACT ACCAGCCCAATCTGCCGACT ACCAGCCCAATCTGCCGACT ACCAGCCCCAATCTGCCGACT ACCAGCCCCAATCTGCCGACT ACCAGCCCCAATCTGCCGACT ACCAGCCCCAATCTGCCGACT ACCAGCCCCAATCTGCCGACT ACCAGCCCCAATCTGCCGACT ACCAGCCCCAATCCTGCCGACT ACCAGCCCCAATCTGCCGACT ACCAGCCCCAATCCTGCCGACT ACCACCCCCCCCCC		
TAAACTGCTTGCATACGGCG TATAAGCCTTGCAGCGGACC TATAAGCCTTGCAGCGGACC TATAAGCCTTGCAGCGGACC TTAATAGCCTTGAGCAGCGA BO ATAAATGCTTGGAACCCTCG B1 GAAAGTTCATGGAATCGAGC B2 GCAAGGATTTCGACTCAGAC B3 CAAAGAATAATCGCTCCTCG B4 TAAAGCACTTATGACTCGGC B5 TTATAGCATTCTGTAGGCGC B6 TCGCTGACATTTGATTAGCC B7 CCTTGAATAATATCTCGGCC B8 AGGTCCAGAAATTGCTGCAC B9 AGCTCAGGAAATTGCTGCAC B9 AGCTCAGGAAATTCTAGCGA 90 AGCTATGCAAATTAGGCC 91 GGTAGGCTAATTTATGGCAC 92 CTAATGCAATTCAATGCCGC 93 CAACTGCAATCAATACGCT 94 CCAAGCGAATCAATACGCT 95 GCATAGCGAATTGGAGATAC 96 GCATGTCGAATGGAGATAC 97 GCACGTTCAATGGCTCGACT 98 GCACGCCAATCTGTCGAGTA 99 AGCAGTGCAAATCCTGATAC		
TATAAGCCTTGCAGCGGACC TRATAAGCGTTGAGCTTAGCT TTAATAGCCTTGAGCAGCGA BO ATAAATGCTTGGAACCCTCG B1 GAAAGTTCATGGAATCGAGC B2 GCAAGGATTTCGACTCAGAC B3 CAAAGAATAATCGCTCCTCG B4 TAAAGCACTTATGACTCGGC B5 TTATAGCATTCTGTAGGCGC B6 TCGCTGACATTTGATTAGCC B7 CCTTGAATAATATCTCGGCC B8 AGGTCCAGAAATTGCTGCAC B9 AGCTCAGGAAATTGCTGCAC B9 AGCTATGCAAATTAGAGCC 91 GGTAGGCTAATTTATGGCAC 92 CTAATGCAATTCAATGCCGC 93 CAACTGGCAATCAATACGCT 94 CCAAGCGAATCAATACGCT 95 GCATAGCGAATTGGAGATAC 96 GCATGTCGAATGGAGATAC 97 GCACGTTCAATGGCTCGACT 98 GCACGCCAATCTGTCGAGTA 99 AGCAGTGCAAATCCTGATAC		
TTTAAGCGGTGGATCTAGCT TTAATAGCCTTGAGCAGCGA ATAAATGCTTGGAACCCTCG B1 GAAAGTTCATGGAATCGAGC B2 GCAAGGATTTCGACTCAGAC B3 CAAAGAATAATCGCTCCTCG B4 TAAAGCACTTATGACTCGGC B5 TTATAGCATTCTGTAGGCGC B6 TCGCTGACATTTGATTAGCC B7 CCTTGAATAATATCTCGGCC B8 AGGTCCAGAAATTGCTGCAC B9 AGCTCAGGAAATTGCTGCAC B9 AGCTATGCAAATTAGAGCC 91 GGTAGGCTAATTTATGGCAC 92 CTAATGCAATTCATGCGC 93 CAACTGGCAATCAATCCGC 94 CCAAGCGAATCAATCCGC 95 GCATAGCGAATTGGAGATAC 96 GCATGTCGAATTGGAGATAC 97 GCACGTTCAATGGCTCGACT 98 GCACGCCAATCTGTCGAGTA 99 AGCAGTGCAAATCTGCGCT		
TTAATAGCCTTGAGCAGCGA ATAAATGCTTGGAACCCTCG ATAAATGCTTGGAACCCTCG ATAAATGCTTGGAACCCTCG ACAAGAATTCATGGAATCGAGC ACAAGAATAATCGCTCCTCG ACAAGCACTTATGACTCGGC ACAAGCACTTATGACTCGGC ACACTTCTGTAGGCGC ACCTTGACATTTGATTAGCC ACCTTGAATAATATCTCGGCC ACCTTGAATAATATCTCGGCC ACCTTGAATAATTCTAGCGA ACCTCAGGAAATTCTAGCGA ACCTCAGGAAATTCTAGCGA ACCTATGCAAATTATGCCC ACCTTGAATAATTATGCCC ACCTTGAATAATTATGCCC ACCTTGAATAATTCTAGCGA ACCTATGCAATTCAATGCCCC ACCTTGAATTCAATGCCCC ACCTATGCAATTCAATACCCT ACCTAGCGAATCAATACCCT ACCTAGCGAATTGAGATACC ACCTAGCGAATTGAATACCCT ACCTAGCGAATTGAATACCCT ACCTTCAATGGCTCGACT ACCACGTTCAATGGCTCGACT ACCACGCCAATCTGTCGAGTA ACCACGTGCAAATCCTGATAC ACCACGTGCAAATCCTGATAC		
80 ATAAATGCTTGGAACCCTCG 81 GAAAGTTCATGGAATCGAGC 82 GCAAGGATTTCGACTCAGAC 83 CAAAGAATAATCGCTCCTCG 84 TAAAGCACTTATGACTCGGC 85 ITATAGCATTCTGTAGGCGC 86 TCGCTGACATTTGATTAGCC 87 CCTTGAATAATATCTCGGCC 88 AGGTCCAGAAATTGCTGCAC 89 AGCTCAGGAAATTCTAGCGA 90 AGCTATGCAAATTAGAGGCC 91 GGTAGGCTAATTTATGGCAC 92 CTAATGCAATTCAATGCCGC 93 CAACTGGCAATCAATGCCGC 94 CCAAGCGAATGCAACGTATC 95 GCATAGCGAATTGAGAGATAC 96 GCATGTCGAATGGAGATAC 97 GCACGTTCAATGGCTCGACT 98 GCACGCCAATCTGCAGTA		
B1 GAAAGTTCATGGAATCGAGC B2 GCAAGGATTTCGACTCAGAC B3 CAAAGAATAATCGCTCCTCG B4 TAAAGCACTTATGACTCGGC B5 TTATAGCATTCTGTAGGCGC B6 TCGCTGACATTTGATTAGCC B7 CCTTGAATAATATCTCGGCC B8 AGGTCCAGAAATTGCTGCAC B9 AGCTCAGGAAATTCTAGCGA 90 AGCTATGCAAATTAGAGGCC 91 GGTAGGCTAATTTATGGCAC 92 CTAATGCAATTCAATGCCGC 93 CAACTGGCAATCAATACGCT 94 CCAAGCGAATCAATACGCT 95 GCATAGCGAATTGGAGATAC 96 GCATGTCGAATGGAGATAC 97 GCACGTTCAATGGCTC 98 GCACGCCAATCTGCAGTA 99 AGCAGTGCAAATCCTGATAC		
B2 GCAAGGATTTCGACTCAGAC B3 CAAAGAATAATCGCTCCTCG B4 TAAAGCACTTATGACTCGGC B5 TTATAGCATTCTGTAGGCGC B6 TCGCTGACATTTGATTAGCC B7 CCTTGAATAATATCTCGGCC B8 AGGTCCAGAAATTGCTGCAC B9 AGCTCAGGAAATTCTAGCGA 90 AGCTATGCAAATTAGAGGCC 91 GGTAGGCTAATTTATGGCAC 92 CTAATGCAATTCAATGCCGC 93 CAACTGGCAATCAATACGCT 94 CCAAGCGAATCAATACGCT 95 GCATAGCGAATTGAGAGATAC 96 GCATGTCGAATGGAGATAC 97 GCACGTTCAATGGCTCGACT 98 GCACGCCAATCTGCGACT 99 AGCAGTGCAAATCCTGATAC		
83 CAAAGAATAATCGCTCCTCG 84 TAAAGCACTTATGACTCGGC 85 TTATAGCATTCTGTAGGCGC 86 TCGCTGACATTTGATTAGCC 87 CCTTGAATAATATCTCGGCC 88 AGGTCCAGAAATTGCTGCAC 89 AGCTCAGGAAATTCTAGCGA 90 AGCTATGCAAATTAGAGGCC 91 GGTAGGCTAATTTATGGCAC 92 CTAATGCAATTCAATGCCGC 93 CAACTGGCAATCAATACGCT 94 CCAAGCGAATCAATACGCT 95 GCATAGCGAATTGGAGATAC 96 GCATGTCGAATGGAGATAC 97 GCACGTTCAATGGCTCGACT 98 GCAGCGCAATCTGTCGAGTA 99 AGCAGTGCAAATCCTGATAC		
84 TAAAGCACTTATGACTCGGC 85 TTATAGCATTCTGTAGGCGC 86 TCGCTGACATTTGATTAGCC 87 CCTTGAATAATATCTCGGCC 88 AGGTCCAGAAATTGCTGCAC 89 AGCTCAGGAAATTCTAGCGA 90 AGCTATGCAAATTAGAGGCC 91 GGTAGGCTAATTTATGGCAC 92 CTAATGCAATTCAATGCCGC 93 CAACTGGCAATCAATACGCT 94 CCAAGCGAATGCAACGTATC 95 GCATAGCGAATTGAGGATAC 96 GCATGTCGAATGGAGATAC 97 GCACGTTCAATGGCTCGACT 98 GCAGCGCAATCTGTCGAGTA 99 AGCAGTGCAAATCCTGATAC		
85 TTATAGCATTCTGTAGGCGC 86 TCGCTGACATTTGATTAGCC 87 CCTTGAATAATATCTCGGCC 88 AGGTCCAGAAATTGCTGCAC 89 AGCTCAGGAAATTCTAGCGA 90 AGCTATGCAAATTAGAGGCC 91 GGTAGGCTAATTTATGGCAC 92 CTAATGCAATTCAATGCCGC 93 CAACTGGCAATCAATACGCT 94 CCAAGCGAATGCAACGTATC 95 GCATAGCGAATTGGAGATAC 96 GCATGTCGAATGGATGATAC 97 GCACGTTCAATGGCTCGACT 98 GCACGCCAATCTGCAGTA 99 AGCAGTGCAAATCCTGATAC	}	
86 TCGCTGACATTTGATTAGCC 87 CCTTGAATAATATCTCGGCC 88 AGGTCCAGAAATTGCTGCAC 89 AGCTCAGGAAATTCTAGCGA 90 AGCTATGCAAATTAGAGGCC 91 GGTAGGCTAATTTATGGCAC 92 CTAATGCAATTCAATGCCGC 93 CAACTGGCAATCAATACGCT 94 CCAAGCGAATGCAACGTATC 95 GCATAGCGAATTGGAGATAC 96 GCATGTCGAATGGATGATAC 97 GCACGTTCAATGGCTCGACT 98 GCAGCGCAATCTGTCGAGTA 99 AGCAGTGCAAATCCTGATAC		
87 CCTTGAATAATATCTCGGCC 88 AGGTCCAGAAATTGCTGCAC 89 AGCTCAGGAAATTCTAGCGA 90 AGCTATGCAAATTAGAGGCC 91 GGTAGGCTAATTTATGGCAC 92 CTAATGCAATTCAATGCCGC 93 CAACTGGCAATCAATACGCT 94 CCAAGCGAATGCAACGTATC 95 GCATAGCGAATTGAGAGATAC 96 GCATGTCGAATGGAGATAC 97 GCACGTTCAATGGCTCGACT 98 GCAGCGCAATCTGTCGAGTA 99 AGCAGTGCAAATCCTGATAC	86	L 1
89 AGCTCAGGAAATTCTAGCGA 90 AGCTATGCAAATTAGAGGCC 91 GGTAGGCTAATTTATGGCAC 92 CTAATGCAATTCAATGCCGC 93 CAACTGGCAATCAATACGCT 94 CCAAGCGAATGCAACGTATC 95 GCATAGCGAATTGGAGATAC 96 GCATGTCGAATGGATACC 97 GCACGTTCAATGGCTCGACT 98 GCAGCGCAATCTGTCGAGTA 99 AGCAGTGCAAATCCTGATAC	87	
89 AGCTCAGGAAATTCTAGCGA 90 AGCTATGCAAATTAGAGGCC 91 GGTAGGCTAATTTATGGCAC 92 CTAATGCAATTCAATGCCGC 93 CAACTGGCAATCAATACGCT 94 CCAAGCGAATGCAACGTATC 95 GCATAGCGAATTGGAGATAC 96 GCATGTCGAATGGATACC 97 GCACGTTCAATGGCTCGACT 98 GCAGCGCAATCTGTCGAGTA 99 AGCAGTGCAAATCCTGATAC	88	AGGTCCAGAAATTGCTGCAC
91 GGTAGGCTAATTTATGGCAC 92 CTAATGCAATTCAATGCCGC 93 CAACTGGCAATCAATACGCT 94 CCAAGCGAATGCAACGTATC 95 GCATAGCGAATTGGAGATAC 96 GCATGTCGAATGGATGATAC 97 GCACGTTCAATGGCTCGACT 98 GCAGCGCAATCTGTCGAGTA 99 AGCAGTGCAAATCCTGATAC	89	
91 GGTAGGCTAATTTATGGCAC 92 CTAATGCAATTCAATGCCGC 93 CAACTGGCAATCAATACGCT 94 CCAAGCGAATGCAACGTATC 95 GCATAGCGAATTGGAGATAC 96 GCATGTCGAATGGATGATAC 97 GCACGTTCAATGGCTCGACT 98 GCAGCGCAATCTGTCGAGTA 99 AGCAGTGCAAATCCTGATAC	90	AGCTATGCAAATTAGAGGCC
93 CAACTGGCAATCAATACGCT 94 CCAAGCGAATGCAACGTATC 95 GCATAGCGAATTGGAGATAC 96 GCATGTCGAATGGATAAC 97 GCACGTTCAATGGCTCGACT 98 GCAGCGCAATCTGTCGAGTA 99 AGCAGTGCAAATCCTGATAC	91	
93 CAACTGGCAATCAATACGCT 94 CCAAGCGAATGCAACGTATC 95 GCATAGCGAATTGGAGATAC 96 GCATGTCGAATGGATAAC 97 GCACGTTCAATGGCTCGACT 98 GCAGCGCAATCTGTCGAGTA 99 AGCAGTGCAAATCCTGATAC	92	
94 CCAAGCGAATGCAACGTATC 95 GCATAGCGAATTGGAGATAC 96 GCATGTCGAATGGATGATAC 97 GCACGTTCAATGGCTCGACT 98 GCAGCGCAATCTGTCGAGTA 99 AGCAGTGCAAATCCTGATAC	93	
95 GCATAGCGAATTGGAGATAC 96 GCATGTCGAATGGATGATAC 97 GCACGTTCAATGGCTCGACT 98 GCAGCGCAATCTGTCGAGTA 99 AGCAGTGCAAATCCTGATAC	94	
96 GCATGTCGAATGGATGATAC 97 GCACGTTCAATGGCTCGACT 98 GCAGCGCAATCTGTCGAGTA 99 AGCAGTGCAAATCCTGATAC	95	
97 GCACGTTCAATGGCTCGACT 98 GCAGCGCAATCTGTCGAGTA 99 AGCAGTGCAAATCCTGATAC	96	
98 GCAGCGCAATCTGTCGAGTA 99 AGCAGTGCAAATCCTGATAC	97	
99 AGCAGTGCAAATCCTGATAC	98	
		······································
	100	

Seq. Id	3' to 5' sequence
101	AGCCTGCGAAATCTACTGAA
102	GCAGATCGAATTATGGAGAC
103	GCAGAGTCAATTATCATGCC
104	CGTTAGGCAATACATTTCCC
105	ACTGGTGCAAAGTCTTCGAC
106	GGTATATGAATGTGTCGTCC
107	GATAGTGCAATCTAGGTGAC
108	GCAGTGCAATGGATGTACTA
109	GCTAGGCTAATGTCCGGCTA
110	GGTAGCCTAATGTGTGCTCA
111	GGACGTGCAATCTTGTGACC
112	GAGCGCCGAATCTAGTCGAA
113	GGGAGCGACCTCTAGCTTAT
114	GCGGGTCGAATCTCGCTTAA
115	CGCCGCGCAAGCTGTATTAA
116	CGGCTGCGAAGCTGTCTTAA
117	CATCCGCTAAGATCGGTTAA
118	CGTGCAGCATAATCCATCAG
119	TGAGAGCTGGATCGCATTCC
120	TAGGTGCTAGGATCTCAGCC
121	TAGGTATCAGGATTCAGGCC
122	TGCGCCAGTGAGTCGTATAT
123	CAGCAACGTGGATCAACTAT
124	CAGCGGCTAAGATCAATACC
125	GCAGCCTAATCTGGCCTAGT
126	GGGCCTGTACCTGCAATTCA
127	TAGGCCGGACCTGCTGTTAT
128	TAAGCCGCCACGGAGTGTTA
129	TAAGGCTCTTGAGACGTAGT
130	TAAGCCCGATCAGCATGGAC
131	TTGCCCGTAGTCAGCTTAGA
132	GAAGCACCGATCAGACACTG
133	CAGGCACCAAGTAGCACAGT
134	GGTGCGCCATGTACTCAGTT
135	TCAGGCTTATCGAGCGCGTT
136	GCAGGCAGATCGACCTAGTT
137	GGATAGGGACTCAGATATAC
138	GCATGGTTACCTACGCCAGA
139	GGAGGCTGACTCATACGCAA
140	GGAGCCTGACCTAGTCGATA
141	GCGGCCAATTCGGCGATAAT
142	GGTGCTCGACATTAGGCCAT
143	GATCCCACATAGCGGACAAT
144	GATCCAATCTGTCAGCACAT
145	GAGCCAATCTGACTACCAGT
146	TGCTGGATATGACTGTCGTA
147	TGCTCTGCACTGCTGACGTA
148	TCACCAGCCAGACTGTGTAG

Seq. Id	3' to 5' sequence
149	AGGAGCAACCATCATGCACG
150	GGGCATACCTATCCCGAGAT
151	CGGGCGATACCACTCAGATT
152	AGCGGCAACCAGACATACGT
153	CACGCCATACCAAGGAGAGT
154	CAGTGCATACCAAGCGACGA
155	CAGGCAGTACACAATCTACG
156	TACGTCGCATCCATAGCTGA
157	GAGTGACACCTCAGCAGATA
158	CTACAGCACCTCAGGAGAGT
159	CTCACGACATCCAGGAGTAT
160	CCAGCACGACAGAGATGT
161	CGCACACCTGAGAGAGAT
162	GCGCACGCACTCAGATGTAA
163	AGACGCTCAACCACGAGAGT
164	GACGCCACAGTCACTAGAGA
165	GGCGCACACTGTACTCAGAT
166	CGAAGCGCCAGTACCAGATA
167	GGGTCGCTACCTACTCTGAT
168	GAGACATGATCTACCAGTAC
169	GGACGCTTACTCAGCAGTCA
170	CGGGTGTTACAGAGCTATCA
171	CGCGGCTTACACAGACATTA
172	CGGAGCTTACACATTAGCAG
173	CTGAGCATACACTTCACGAT
174	CCGATCATAACTGTAGATGC
175	CCGCCGATAACTGCTTGAGA
176	GGCCATATACGAGATGTAGA
177	CGTCCCTTAACGGCTGGTAT
178	ATACCCAGAACGACTATGCG
179	ATCCCACGAACGATGAATCT
180	ATCCGCAGAACCGGCGATAA
181	CCTCGCCGAAGCGTGTTTAA
182	GCGCCGCACAGAGTCTTATA
183	CGCGCTGCACAGAGCATATA
184	CCGCTGACACAGGCAGATAT
185	GCGTATGACCAGGTGTATAT
186	CTGTATGAAGGTGCTGTACT
187	GTTTCGCACGAGGATGTATC
188	GTGCTCGCAGAGGATTTATC
89	TAGGCCAGAGTAGCGACTTA
90	CAGATCCTAAGAGCAGTTAC
91	TAGATGCTAGGAGCGATTCA
92	TAAGTCGGTGGAGCATTCA
93	TAAGCGCGTGGACTCCTAAA
95	TAAGTGGACTGAGCGCATAT
	TATACGGCAGTGGATCAGAT
96	CTATACGCAATGCACTCAGA

Seq. Id	3' to 5' sequence
197	CTATCGTCAAGTGATGGACC
198	TATAGACTAGGTGATCGAGC
199	TAGTACGAGTGGGCATCAAA
200	TAGACGTAGTGAGCATGACT
201	TGACGAGTTAGGATCTATGC
202	TTACGAGTGTAGCGTCCATG
203	TCGTCGTAGCATCTCGCAGT
204	TCGACGTAGGATCGCAGTAC
205	TCAGTATCATGGAGTACGAG
206	TGCACTAGATGGGATCGACT
207	TGCGATTACTGCCGTCACGT
208	TGGACTCTATGGCAGCCGTA
209	TGACAGCAGTTGCAGTCCGT
210	TACACAGGCTTGCAGCTCGA
211	TGCAGCGGAGTGCCTCATTA
212	GCGCAGGGAGATCCATATCA
213	CGGCAGCCAAGTCCAGTATA
214	CAGCGCCCAAGACGTGTATA
215	GTGCCTGCATAGCGATAGTC
216	TGCCTGCGAGAGCCTGTATT
217	TGGCATCGAGAGCCGTTCTA
218	GCAGGAGCAGAGCTTATATC
219	GCGGGATCACGACGTTTACA
220	GTGGCGATAGAGCATTCTCC
221	AACGCGAGAAACCATTTGCC
222	AGGCAGACAACTCAATCCGG
223	AGGAGAGCAACCTACACTCG
224	AGCCAACGAACCTACATGGG
225	CCGCAAGCACGTCGAATGAA
226	GCGCATGGACGACAACGTA
227	GCCAGGAGACGTAGATATTA
228	GCGCATAGAGAGATCATC
229	TGGTATATCGGTAGATTCGC
230	GAGCTATAAGGTGGATTCAC
231	CGCGGATAACTTGATTCACC
232	GTCGGCTTACCTGATAGCGA
233	GGAGCTATACATGCCTATCC
234	GGTGCCGTACATGCTCGTAT
235	TCGGCTTGACGTGCTCGTAT
236	GGGCTGTGACTAGACTCTCA
237	GCGAATTTAGTAGACGCACA
238	GAATCTCGAATAGCGGTACA
239	GACAGTTGACATGACAGTAG
240	GACATTGACATCGCATACAC
241	GAGTTTAGAATCGTGAGCAC
242	CTATTCGCAAGTGTCGAGCC
243	GTTATGGACACTGCTCGACG
244	AGCGTTCTAAATGCGTCACA
	

Seq. Id	3' to 5' sequence
245	CCGATATGAACTGTCACTAC
246	CGCGAATGAAGTCTACATAC
247	CCACTATGAAGCGATATACC
248	CACCAGTGAAGAGATACCGC
249	GCACTGTTACATGATACCTC
250	GCCAGTTACAGTCATGCCTA
251	GCGCAGCTAGATCCACTGAT
252	GCGTGCGGAGACCTCATTTA
253	GCTCACGAGGCACGCTTTAT
254	GCGCCAGTAGCACGCTTATT
255	GGCTCAGTAGCACTCATCAT
256	ACTTGCACAGCACAATACGT
257	CGCCATACAGCACGATATTA
258	CCGCAGACAGCACGAGTATT
259	CCAAGGAGACTACACGATCT
260	GCACAGGTAGCTCGACGTAT
261	GTCAAGATGCTACCGTTCAG
262	CGATATGAAGCTCAGTGAAC
263	CCTATGAAGCTATCGCAACA
264	CTTATCACAGCATCCGAGAG
265	CCCGTGCAACGATTTGACAA
266	CGGCGGTTAAGTTCTAATCA
267	GGTCGAGCATGATAGCTTAT
268	GTGGTAGCAGCATAGCTTAT
269	TAGCGTGGAGCATCCTCAGT
270	CAACGGTGAGCAACTATCAG
271	CTGGTTCGAGCAATCTATCA
272	TCGGGTCTAGGATGCTCTAC
273	TCGATGCACTGATGTCACTA
274	TCGTATATCCCATGCGATCT
275	TACGGTCCAGCATCAGCTTA
276	ATCAGTCCAACCTACAGATG
277	ATCAACTGAACCTCATACGG
278	TACTTCTGAGCAGGGAGCTA
279	TAGTTATGAGCAGGCGTCCA
280	CTTGTGACATCAGCCACGAT
281	CACGGAGCAGAGCACATCT
282	CACGGGTGAAGAGCCATACA
283	CAGGAGTTAATAGCTCATCC
284	TAAGATTAGTTAGCAGCGCC
285	GAGTGATTAGCAGCGCC
286	CGATGATTAGCAGACGCCACG
287	GACTGATTACCAATGCCACA
288	GATTATGTAGCACATCCACA
289	GCTATATTACGAGCTATGCCC
290	GTTTATATCGAGGCAGGCCA
	GTTACTATCGAGGCAGGCCA
	CGTCATGTACCATCAGAGCG
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Seq. Id	3' to 5' sequence
293	GTTATCTACGGATCATGCGA
294	CTGCCGTAAGTCTCATGCGA
295	CTAGCCGAATACTGCATACA
296	CTGCGTCGAGAATCGCGTTA
297	CATACACGACAATAGCTTCG
298	GATACCGACTCATACATTGC
299	GATACCGCACGATCAGCAGA
300	GTATATGCAGACTACTGGAG
301	TATAGTCGATTATCCCAGCC
302	CATAGTACAATATCCCGACG
303	CTTGACAGCTACTACCAGTG
304	CTGAGACAGCTATCGACACA
305	CTGAGTAAGTCTTCCACACG
306	TCGGATATACTATGCGTCAG
307	CGTAGGATAGAATGCACAGT
308	CATGATACACACTCACGAGG
309	CGGAATCACGACTACATACG
310	GGGTATCACGAGTCACCTCA
311	GAGAGAATCGTATCACAGCC
312	GAGTATGTAATCTACCTGCC
313	GAGTAATCATAGTAGCAGCC
314	GACTATATCCAGCACCGAGG
315	GACATATAGCTCCACTCAGA
316	TAGACCTAGTTGCAGCGCGA
317	TACTACACGTTTCACGGCAG
318	GTACATATCTGTCACGCGCA
319	TAGTATATCCTACGCCGCTA
320	GAGTATATCGCAATGCCAGC
321	GAGTTGTCACATAGGCCACC
322	GACGCATGACATATTCCTAC
323	GAGACACTTGACAGTAGCCA
324	GGCTAGTTACTCAGATCACA
325	CGCAATAAGTCTAGCTCACT
326	CATGTACTAAGCAGTCACAC
327	CTAGTTAATGTCAATCCGGC
328	GACTGTGTAATCATTGCAGC
329	CGTTCGTGAATCAGCACAGC
330	ATTCGGTCACACAGCACAGA
331	ATCTGCTGACACACACTAAG
332	AGCTCGCTAAATATGTAGGC
333	ACTGTCGCAAATATCACACG
334	ACTGTCTGACCAACCAATAG
335	GTTACTAGCTGGACCTCAGA
336	TTATAGACTGGTGCGGAACA
337	TTAGCATACTGTGCGCGAAC
337 338	TGTGCTGACTTAGGTCGAAT
339	TCTCGGGACGTTGCGCTATA
340	TGTCCGCGACGTTGGCTATA

TGTTCGTGACTGTGCGCTAC 342 TGTCAGGTACTGGTCGCTAC 343 TTCATGTACTGTGGCTACCG 344 TTTACTAGAGTGGCGCATGA 345 TTAGATAGATGTCGGCCAG 346 CTCAATAGATTATAGGCGCG 347 TCGAATCGCTGTTACGGAAA 348 TCAGACTAGGGTAGCGCATA 349 TCAGCAGTATGTAGGCAGTA 350 TAAGCCGGGTCACGCTATTT 351 TATGACCGATGTGCAGGTAT 352 TTAGCACGCTCGCGAGTAT 353 TTCACACGGTCGCGAGTAT 354 CTTCAGACAGAGAGAAA 355 TCCAGCGACGTCGCGATTA 356 TCCAGCCGACGTCTGCAGCTTA 357 CTCCAGCCGACGTCTGAG 358 CTCCAGCGACGTCTGAG 359 TGTCAGCGGACTCCGCATATA 360 TCCATGCGAGATCAGAAA 361 TGCAAGCAGTACTGCAGAAA 362 TGTAGGACCTCGCCATATA 361 TGCAAGCAGTTCCAGCGTA 362 TGTAGGACCTGTGCCACTG 363 TITATCGCAGTGCTCACTG 364 TATGTCAGCAGGCCCAGCT 365 TTCCTGTAGCTCACCGGT 366 TATTCAGACTAGGACCCATATA 367 TATTATACTGCGAGCCCAGCT 368 GACCTTACACTGGCCCAGCT 370 TCGGATAGCAGGCCCAGAA 371 GCTGATGCAGAGCCCATA 372 GCTGATCACACTGGCCCATA 373 CGCTTTGTACCAGGCCCAAGA 374 CGTGATGCACGAGCCCATA 375 TACGCAGAGCCCATAA 377 TCGGATACCAGGACCCATA 378 CTCCAGCAACTCGCATAA 379 TCGGATCACACGAGCCCAGCT 377 ATCGTTGCACCAGACCACG 377 ATCGTTGCACCAGACCACG 377 ATCGTTGCACCAGACCACG 378 CTCTCAGGACCAGACCACG 379 TCTGAGCGACCAGCACAC 379 TCTGAGCGACCAGCACAC 379 TCTGAGCCACAGCACCACG 380 GGTGAGACCCAGTAC 381 TTAGAGCTTTAGGCATCCA 382 TTATAGCCGTAGGCACCACG 383 CTCTCAAGTATTAGACACCACCA 384 GCTACCAATTAGACCACCAC 385 CTCTCAAGTATTAGACACCACCAC 386 TATTCAACCAGACCACCACACCACCACCACCACCACCACCACCA	Seq. Id	3' to 5' sequence
TITCATGTACTGTGGCTACCG 344 TITACTAGAGTGGCGCATGA 345 TITAGATAGATGTTCGGCCAG 346 CTCAATAGATTATAGGCGCG 347 TCGAATCGCTGTTACGGAAA 348 TCAGACTAGGGTAGCGCATA 349 TCAGCAGTATGTAGGCAGTA 350 TAAGCCGGGTCACGCTATTT 351 TATGACCGATGTGCAGGTAT 352 TTAGCACGTCGGCGATGTT 353 TTCACACGGTCTGCGAGCTT 354 CTTCAGACAGGAGGAGATAT 355 TCCAGCCGACGTCTGCAGCTT 356 TCCAGCCGACGTCTGCAGCTT 357 CTCCAGTCAGGTCTGCAG 358 CTCCAGCGAAGTGATGAGAA 359 TGTCAGCGGATCTCCAAG 360 TCCATGCGAGGATCAGCATATA 361 TGCAAGCAGTCTCCACTG 362 TGTAGGACCTGGCCATATA 363 TTTATCCAGCGGATCACCATATA 364 TATGTCAGCAGTCTCACTG 365 TTCCTCTGAGAGACTCTCACTG 366 TATTCGAGCTGCCCAGTT 367 TATTTATACTGCAGGCCCAGCT 368 GACCTTACACTGGCCCAGT 369 TACTGAGACAGTCCCAGTA 370 TCGGATAGCAGGCCAGAG 369 TACTGATAGCATGCGCCTAA 371 GCTGATGCAGGACCACTA 372 GCTGGATCACCAGGCCCATA 373 CGCTTTGTACCAGGCCCATA 374 CGTGATGCACGAGCCCATA 375 TACGCTGGATCACAGGCCCATA 376 ATCCGAACCAGACCCAGT 377 ATCGTACCAGGCCCATA 378 CTCCAGCAACACACACA 379 TCCAGACCAGACCCAGT 370 TCGGATCACAGACCCAGT 371 GCTGATGCACAGACCCAGT 372 GCTGGATCACAGAGCCCATA 373 CGCTTTGTACCAGGCCCATA 374 CGTGATGCACAGACCCAGT 375 TACGCTGGATCACAGACCCAGT 376 ATCCTGAACCAGACCCAGT 377 ATCGTTGCACCAGACCCAGT 378 CTCTCAGGACCAGAACACCA 379 TCTGAGCGACCAGAACACA 380 GGTGAGACCTTAGGCACGCAG 381 TTAGAGTCTTAGGCATGTCC 382 TTATAGCCGTAGGCACGCA 384 GCTAGGATATAGGACACTGA 385 GCTATCGAATGTGCAGTACCA 386 GCTATCGAATGTGCAGTACCA 387 CTCTAAGTATTGGACACCACACACACA 388 GCTATCGAATGTGCAGTACCA 388 GCTATCGAATGTGCAGTACCACA 388 GCTATCGAATGTGCAGTACCA 388 GCTATCGAATGTGCAGTACCA 388 GCTATCGAATGTGCAGTACCA 388 GCTATCGAATGTGCAGTACCACACACACACACACACACAC	341	TGTTCGTGACTGTGCGCTAC
TITCATGTACTGTGGCTACCG 344 TITACTAGAGTGGCGCATGA 345 TITAGATAGATGTTCGGCCAG 346 CTCAATAGATTATAGGCGCG 347 TCGAATCGCTGTTACGGAAA 348 TCAGACTAGGGTAGCGCATA 349 TCAGCAGTATGTAGGCAGTA 350 TAAGCCGGGTCACGCTATTT 351 TATGACCGATGTGCAGGTAT 352 TTAGCACGTCGGCGATGTT 353 TTCACACGGTCTGCGAGCTT 354 CTTCAGACAGGAGGAGATAT 355 TCCAGCCGACGTCTGCAGCTT 356 TCCAGCCGACGTCTGCAGCTT 357 CTCCAGTCAGGTCTGCAG 358 CTCCAGCGAAGTGATGAGAA 359 TGTCAGCGGATCTCCAAG 360 TCCATGCGAGGATCAGCATATA 361 TGCAAGCAGTCTCCACTG 362 TGTAGGACCTGGCCATATA 363 TTTATCCAGCGGATCACCATATA 364 TATGTCAGCAGTCTCACTG 365 TTCCTCTGAGAGACTCTCACTG 366 TATTCGAGCTGCCCAGTT 367 TATTTATACTGCAGGCCCAGCT 368 GACCTTACACTGGCCCAGT 369 TACTGAGACAGTCCCAGTA 370 TCGGATAGCAGGCCAGAG 369 TACTGATAGCATGCGCCTAA 371 GCTGATGCAGGACCACTA 372 GCTGGATCACCAGGCCCATA 373 CGCTTTGTACCAGGCCCATA 374 CGTGATGCACGAGCCCATA 375 TACGCTGGATCACAGGCCCATA 376 ATCCGAACCAGACCCAGT 377 ATCGTACCAGGCCCATA 378 CTCCAGCAACACACACA 379 TCCAGACCAGACCCAGT 370 TCGGATCACAGACCCAGT 371 GCTGATGCACAGACCCAGT 372 GCTGGATCACAGAGCCCATA 373 CGCTTTGTACCAGGCCCATA 374 CGTGATGCACAGACCCAGT 375 TACGCTGGATCACAGACCCAGT 376 ATCCTGAACCAGACCCAGT 377 ATCGTTGCACCAGACCCAGT 378 CTCTCAGGACCAGAACACCA 379 TCTGAGCGACCAGAACACA 380 GGTGAGACCTTAGGCACGCAG 381 TTAGAGTCTTAGGCATGTCC 382 TTATAGCCGTAGGCACGCA 384 GCTAGGATATAGGACACTGA 385 GCTATCGAATGTGCAGTACCA 386 GCTATCGAATGTGCAGTACCA 387 CTCTAAGTATTGGACACCACACACACA 388 GCTATCGAATGTGCAGTACCA 388 GCTATCGAATGTGCAGTACCACA 388 GCTATCGAATGTGCAGTACCA 388 GCTATCGAATGTGCAGTACCA 388 GCTATCGAATGTGCAGTACCA 388 GCTATCGAATGTGCAGTACCACACACACACACACACACAC	342	
TITACTAGAGTGGCGCATGA TIAGATAGATGTTCGGCCAG TIAGATAGATGTTCGGCCAG TCGAATCGCTGTTACGGAAA TCGAATCGCTGTTACGGAAA TCAGACTAGGGTAGCGCATA TCAGACTAGGGTAGCGCATA TCAGCCGGGTCACCGCATA TAGCCGGGTCACGCATATT TAGACCGGTCACGCTATTT TATGACCGATGTGCAGGATAT TAGACCGGTCGCGCGATGTT TAGACCGGTCGCGCGATGTT TAGACCGGTCGCGCGATGTT TAGACACGCTCGCGCGATGTT TCACACGGTCTCGCAGCTT TCAGACAGGACGTGCGATTTA TCAGACAGGACGTGCGATTTA TCAGACCGGACGTGCGATTTA TCAGACCGGACGTGCGATTTA TCAGCCGACGTGCGATTTA TCAGCCGACGTGCGATTTA TCAGCCGACGTGCGATTTA TCAGCGGACGTGCCATATA TCAGCGGAACTGATGAGAA TCCAGCGAAGTGATGAGAA TGCAAGCAGTTCTCAGCGTA TGCAAGCAGTTCTCAGCGTA TATTACGCAGTGCTCACTG TATTACGCAGTGCTCACTG TATTCGAGCTAGGCCCAGCTT TATTCAGCTAGCGCCAGCT TATTCAGCTAGCGCCAGCT TATTTATACTGCGAGCCCAGCT TATTTATACTGCGAGCCCAGCT TATTTATACTGCGAGCCCAGCT TCAGATAGCATGGGACGATA TCAGATAGCATGGGACGATA TCAGATAGCATGGGACCATTA TCAGATAGCATGGGACCCATTA TCAGATAGCATGGGACCCATTA TCAGATAGCATGGGACCCATTA TCAGATAGCATGGCACGAGA TCATGATAGCATGGGACCCATTA TCAGATAGCAGGCCCATAC TCAGATAGCAGAGCCCATAC TCAGATGACCAGAGCCCATAC TCAGATTGACCAGAGCCCATAC TCAGATTGACCAGAGCCCATAC TCAGATTGACCAGAGCCCATAC TCAGATTGACCAGAGCCCATAC TCAGATTGACCAGACCCAGT TACCTTGACCAGACCCAGT TACCTTGACCAGACCCAGT TACCTTGACCAGACCCAGT TACCTTGACCAGACCCAGACCCAG TACCTGAACCCAGAACTACA TCAGAGCACTACACACCAGACCCAG TACCTGAACCCAGAACTACA TCAGAGCATCTCCCAGTCA TCAGAGCATCTACACCAGACCCAG TTATAGCCGTAGGCAGGACCCAG TTATAGCCGTAGGCAGGTAC TCAGAGCATCTACACCAGACCCAG TTATAGCCGTAGGCAGGTAC TCAGAGCATATAACGACAGCAGACCCAG TTATAGCCGTAGGCAGGTAC TTATAGCCGTAGGCAGGTAC TTATAGCCGTAGGCAGGTAC TTATAGCCGTAGGCAGCACCCAG TTATAGCCGTAGGCACCAGAACCCAG TTATAGCCGTAGGCAGCACCCAGA TTATAGCCGTAGGCAGCACCCAGA TTATAGCCGTAGGCAGCACCCAGA TTATAGCCGTAGGCAGCACCCAGA TTATAGCCGTAGGCACCCAGACCCAGA TTATAGCCGTAGGCAGCACCCAGA TTATAGCCGTAGGCAGCACCCAGA TTATAGCCGTAGGCAGCACCCAGA TTATAGCCGTAGGCAGCACCCAGA TTATAGCCGTAGGCAGCACCCAGA TTATAGCCGTAGGCAGCACCCAGA TTATAGCCGTAGGCAGCACCAGAACCCCAG TTATAGCCGTAGGCAGCACCCAGA TTATAGCCGTAGGCAGCACCAGAACCCAGA TTATAGCCGTAGCACACCACAC	343	
346 CTCAATAGATTATAGGCGCG 347 TCGAATCGCTGTTACGGAAA 348 TCAGACTAGGGTAGCGCATA 349 TCAGCAGTATGTAGGCAGTA 350 TAAGCCGGGTCACGCTATTT 351 TATGACCGATGTGCAGGTAT 352 TTAGCACGCTCGGCGATGTT 353 TTCACACGGTCTGCGAGCTT 354 CTTCAGACAGGAGGAGATAT 355 TCCAGCCGACGTGTGAGGAGATAT 356 TCCAGCCGACGTGCGATTTA 357 CTCCAGTCAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGA	344	<u> </u>
TCGAATCGCTGTTACGGAAA TCAGACTAGGGTAGCGCATA TCAGACTAGGGTAGCGCATA TCAGCAGTATGTAGGCAGTA TCAGCAGTATGTAGGCAGTA TAGCCGGGTCACGCTATTT TATGACCGATGTGCAGGTAT TATGACCGATGTGCAGGTAT TAGCACGCTCGGCGATGTT TAGCACGGTCTGCGAGCTT TCACACGGTCTGCGAGCTT TCAGACAGGAGGAGAGATAT TCAGACAGGAGGAGAGATAT TCAGACAGGAGGAGGAGATAT TCAGACAGGAGGAGGAGATAT TCAGACAGGAGCTGCGATTTA TCAGACAGGAGAGGAG	345	TTAGATAGATGTTCGGCCAG
TCGAATCGCTGTTACGGAAA TCAGACTAGGGTAGCGCATA TCAGACTAGGGTAGCGCATA TCAGCAGTATGTAGGCAGTA TCAGCAGTATGTAGGCAGTA TAGCCGGGTCACGCTATTT TATGACCGATGTGCAGGTAT TATGACCGATGTGCAGGTAT TAGCACGCTCGGCGATGTT TAGCACGGTCTGCGAGCTT TCACACGGTCTGCGAGCTT TCAGACAGGAGGAGAGATAT TCAGACAGGAGGAGAGATAT TCAGACAGGAGGAGGAGATAT TCAGACAGGAGGAGGAGATAT TCAGACAGGAGCTGCGATTTA TCAGACAGGAGAGGAG	346	CTCAATAGATTATAGGCGCG
TCAGCAGTATGTAGGCAGTA TAAGCCGGGTCACGCTATTT TATGACCGATGTGCAGGTAT TATGACCGATGTGCAGGTAT TTAGCACGCTCGGCGATGTT TTAGCACGCTCGGCGATGTT TTCACACGGTCTGCGAGCTT TCAGACAGGACAG	347	
TAAGCCGGGTCACGCTATTT 351 TATGACCGATGTGCAGGTAT 352 TTAGCACGCTCGGCGATGTT 353 TTCACACGGTCTGCGAGCTT 354 CTTCAGACAGGAGGAGATAT 355 TCCAGCCGACGTGCGATTTA 356 TCCAGCCGACGTGCCATTTA 357 CTCCAGTCAAGTGCTTCGAG 357 CTCCAGTCAAGTGCTTCGAG 358 CTCCAGCGAAGTGATGAGAA 359 TGTCAGCGGATCACGCATATA 360 TCCATGCGAGGATCAGGTAT 361 TGCAAGCAGTTCTCAGCGTA 362 TGTAGGACCTGTCTCACTG 363 TITATCGCAGTGCTCACTG 364 TATGTCAGCAGGCCCAGCTT 365 TTCTCGTAGCTGCGCCTAGT 366 TATTCGAGCTAGGGACGCAT 367 TATTTATACTGCGAGCGAGG 368 GACCTTACACTGGACGAGA 369 TACTGATAGCATGGACGATT 370 TCGGATAGCATGGACGTT 371 GCTGATGCACGAGGCCATTA 372 GCTGGATCACGAGGCCATTA 373 CGCTTTGTACCAGGCCATA 374 CGTGATGCACGAGCCATA 375 TACGCTGGATCAGAGCCAGT 376 ATCCTGAACGAGCCATA 377 ATCGTTGCACCAGACCCAGT 378 CTCTCAGGACCAGACCAGT 379 TCTGAGCCACAGACCCAGT 379 TCTGAGCGATCACA 380 GGTGAGACCTATGATA 379 TCTGAGCGATCAGCAGCAGACCAGA 381 TTAGAGTCTTAGGCATGCG 382 TTATAGCCGTAGGCAGCAGA 384 GCTAGGATATAGGACACTGA 385 GCTATCGAATGTGCAGTACG 386 GCTATCGAATGTGCAGTACG 387 TCTAAGCATTAGGCAGCACAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGCACCCAGACCCAGCACCCAGCACCCAGCACCCAGCACCCAGCACCCAGCACCCAGCACCCAGCACCCCAGCACCCAGCACCCAGCACCCAGCACCCAGCACCCAGCACCCAGCACCCCCAGCACCCCAGCACCCCCAGCACCCCCAGCACCCCCAGCACCCCCAGCACCCCAGCACCCCCAGCACCCCAGCACCCCAGCACCCCAGCACCCCAGCACCCCAGCACCCCAGCACCCCAGCACCCCAGCACCCCAGCACCCCAGCACCCCAGCACCCCAGCACCCCAGCACCCCAGCACCCAGCACCCCAGCACCCCAGCACCCCAGCACCCAGCACCCCAGCACCCAGCACCCCAGCACCCCAGCACCCCAGCACCCAGCACCCCAGCACCCAGCACCCAGCACCCCAGCACCCAGCACCCAGCACCCCAGCACCCCAGCACCCACCCACCA	348	TCAGACTAGGGTAGCGCATA
TATGACCGATGTGCAGGTAT TAGCACGCTCGGCGATGTT TTAGCACGCTCGGCGATGTT TTAGCACGGTCTGCGAGCTT TCACACGGTCTGCGAGCTT TCACACGGTCTGCGAGCTT TCAGCCGACGTGCGATTTA TCCAGCCGACGTGCCGATTTA TCCAGCGACGTACCTGCTTGTAG TCCAGCGAAGTGATGAGAA TCCAGCGAAGTGATGAGAA TCCAGCGAAGTGATCAGGATAT TGCAAGCAGTTCTCAGCGTA TGCAGCGATCAGGTAT TGCAGCGATCAGGTAT TGCAAGCAGTTCTCAGCGTA TTATCGCAGTGCTCACTG TTATCGCAGTGCTCAGCT TATTCGCAGTGCTCAGCTT TTCCGTAGCTGCGCCTAGT TATTCGAGCTAGGACGAGCAT TATTCAGCAGTGCCCAGCTT TATTTATACTGCGAGCGAGG TATTCAACCTGGACCAGAGA TATTTATACTGCGAGCGAGG TACTGATAGCATGCGCCTCTA TCGGATAGCATGCGCCTCTA TCGGATAGCAGTGCGCCTCTA TCGGATGCACGAGGCCATTA TCGGATCACCAGAGCCCATTA TCGGATCACCAGAGCCCATTA TCGCTGGATCACGAGCCCATCA TACCTGAACCAGACCCAGT TACCTGAACCAGACCCAGT TACCTGAACCAGACCCAGT TACCTGAACCAGACCCAGT TCGATTGACCAGACCCAGT TCGAGCCACAGACCCAGT TCGAGCCACAGACCCAGCACACCCAGT TCGAGCCACCAGACCCAGCACCCAGT TCGAGCCACCAGACCCAGCACCCAGCACCCAGCACCCAGCACCCAGCACCCAGCACCCAGCACCCAGCACCCAGCACCCAGCACCCAGCACCCAGCACCCAGCACCCAGCACCCAGCACCCAGCACCCCAGCACCCCAGCACCCAGCACCCCCAGCACCCAGCACCCCAGCACCCCAGCACCCAGCACCCCAGCACCCCAGCACCCAGCACCCAGCACCCCAGCACCCAGCACCCAGCACCCAGCACCCAGCACCCAGCACCCAGCACCCAGCACCCAGCACCCAGCACCCAGCACCCAGCACCCAGCACCCAGCACCCAGCACCCAGCACCCAGCACCAGCACCCAGCACCAC	349	TCAGCAGTATGTAGGCAGTA
TTAGCACGCTCGGCGATGTT TCACACGGTCTGCGAGCTT TCACACGGTCTGCGAGCTT TCAGCCGACGTGCGATTTA TCAGCCGACGTGCGATTTA TCAGCCGACGTGCGATTTA TCAGCCGACGTCGCATTTA TCAGCGGACGTCGCATTTA TCAGCGGACGTCGCATTTA TCAGCGGACGTCGCATTTA TCAGCGGAAGTGATGAGAA TCCAGCGAAGTGATGAGAA TGCAGCGGATCGCCATATA TGCAGCGGATCGCCATATA TGCAAGCAGTTCTCAGCGTA TGCAAGCAGTTCTCAGCGTA TTATCGCAGTGCTCAGCT TATTATCGCAGTGCTCAGGCT TATTCGAGCTGCGCCTAGT TATTTATACTGCGAGCCAGCTT TCGATCGAGCAGCCAGCTT TCGATAGCATGGCACGAGA TATTTATACTGCGAGCCAGAGA TATTTATACTGCGAGCCCATTA TCGATAGCATGGCACCAGAA TCGATAGCACGAGCCCATTA TCGATAGCACGAGCCCATTA TCGATTGACCAGAGCCCATA TCGATTGACCAGACCCATA TACGCTGGATCACAGACCCATA TACGCTGGATCACAGACCCATA TCGATTGACCAGACCCATA TCGATTGACCAGACCCATA TCGATTGACCAGACCCATA TCGATTGACCAGACCCAGACACA TACCTGAACGCAGACCCAGAACTACA TCTCAGACCCAGAACTACA TCTCAGCACCAGACCAG	350	TAAGCCGGGTCACGCTATTT
TTCACACGGTCTGCGAGCTT TCAGACAGGAGAGAGATAT TCAGACAGGAGAGAGATAT TCAGCCGACGTGCGATTTA TCCAGCCGACGTGCGATTTA TCCAGCCGACGTGCGATTTA TCCAGCGACGTGCGATTTA TCCAGCGAAGTGCTTCGAG TCCAGCGAAGTGATGAGAA TGCAGCGGATCGCCATATA TGCAGCGGATCGCCATATA TGCAAGCAGTTCTCAGCGTA TGCAAGCAGTTCTCAGCGTA TTATCGCAGTGCTCAGTCT TATTATCGCAGTGCTCAGGCT TATTCGAGCTGGCCCAGCTT TATTTATACTGCGAGCCAGCT TATTTATACTGCGAGCGAGA TACTGATAGCATGGACGAGA TCCGATAGCATGGACGCTT TCGGATAGCATGGACGCTT TCGGATAGCATGGACGCTTA TCGGATAGCATGGACCCATA TCGGATCACACGAGCCCATA TCGGATCACACGAGCCCATA TCGGATCACACGAGCCCATA TCGGATCACACGAGCCCATA TCGGATCACACGAGCCCATA TCGCTTGACCAGACCCAGT TACCTGAACCAGACCCAGT TACCTGAACGCAGACCCAGT TCCGATCACCAGACCCAGT TCCGATCACCAGACCCAGT TCCGATCACCAGACCCAGT TCCGATCACCAGACCCAGT TCCGATCACCAGACCCAGT TCCGATCACCAGACCCAGT TCCGATCACCAGACCCAGT TCCTCAGGACCAGACTCCA TCCTCAGGACCAGCATCACA TCCTCAGGACCAGCATCACA TCTCAGGACCAGACTCCA TCTCAGGACCAGCATGATA TCTGAGCGATCTGCCAGTCA TCTGAGCGATCTGCCAGTCA TCTGAGCGATCTGCCAGTCA TCTGAGCGATCTGCCAGTCA TCTGAGCGATCTGCCAGTCA TTAGAGCCTTAGGCATGTCG TTATAGCCGTAGGCAGGTAC TTATAGCCGTAGGCAGGTAC TTATAGCCGTAGGCACCCCA TTATAGCCGTAGGCACCCCA TTATAGCCGTAGGCACCCCA TTATAGCCGTAGGCACCCCA TTATAGCCGTAGGCACCCCA TTATAGCCGTAGGCACCCCA TTATAGCCGTAGGCACCCCA TTATAGCCGTAGGCACCCCA TCCAGGATATAGGACACCCCA TTATAGCCGTAGGCACCCCA TTATAGCCGTAGGCACCCCA TCCTCAGGATATAGGACACCCCA TCCTCAGGATATAGGACACCCA TCCTCAGGATATAGGACACCCA TCCTCAGGATATAGGACACCCA TCCTCAGATCATCACACCACCACACCA	351	TATGACCGATGTGCAGGTAT
354 CTTCAGACAGGAGGAGATAT 355 TCCAGCCGACGTGCGATTTA 356 TCCAGCGACGTGCGATTTA 357 CTCCAGTCAAGTGCTTCGAG 358 CTCCAGCGAAGTGATGAGAA 359 TGTCAGCGGATCGCCATATA 360 TCCATGCGAGGATCAGGTAT 361 TGCAAGCAGTTCTCAGCGTA 362 TGTAGGACCTGTGCTCACTG 363 TTTATCGCAGTGCTCAGGCT 364 TATGTCAGCAGGCCAGCTT 365 TTCTCGTAGCTGCCCAGT 366 TATTCGAGCTAGGACGCAT 367 TATTTAACTGCGAGCAGAG 368 GACCTTACACTGGCACGAGA 369 TACTGATAGCATGGACGAT 370 TCGGATAGCATGGACGTT 371 GCTGATGCACGAGGCCATTA 372 GCTGGATCACGAGGCCATA 373 CGCTTTGTACCAGGCCATA 374 CGTGATTGACCAGAGCCATA 375 TACGCTGGATCAGAGCCAGT 376 ATCCTGAACGAGACCCAGT 377 ATCGTTGACCAGACCCAGT 378 CTCTCAGACCCAGAACTACA 379 TCTGAGCCACGAGACTACA 379 TCTGAGCCATGCACGAGACCAGA 380 GGTGAGACCTATGTATATCG 381 TTAGAGTCTTAGGCATGTCG 382 TTATAGCCGTAGGCACCCAGT 383 CTCTAAGTATTGGACACGCA 384 GCTAGGATTAGGACACTGA 385 GCTATCGAATGTGCAGTACG	352	TTAGCACGCTCGGCGATGTT
TCCAGCCGACGTGCGATTTA TCCAGCGTACCTGCTTGTAG TCCAGCGTACCTGCTTGTAG TCCAGCGAAGTGCTTCGAG TCCAGCGAAGTGATGAGAA TGCAGCGGATCGCCATATA TGCAAGCAGGTCACGGTAT TGCAAGCAGTTCTCAGCGTA TGCAAGCAGTTCTCAGCGTA TTATCGCAGTGCTCACTG TTATCGCAGTGCTCAGGCT TTATCGCAGTGCTCAGGCT TTATCGCAGTGCTCAGGCT TTATCGCAGTGCTCAGGCT TATTTATACTGCGAGCCCAGCTT TATTTATACTGCAGCAGGCCAGAG TACTGATAGCATGGCACGAGA TACTGATAGCATGGCACGAGA TACTGATAGCATGGCACCTA TCGGATAGCACGAGCCATTA TCGGATACCACGAGGCCATTA TCGGATCACCAGGCCCATA TCGGATCACCAGAGCCCATA TCGGATCACCAGAGCCCATA TCGCTGGATCACAGACCCAGT TACCTGAACCAGACCCAGT TACCTGAACCAGACCCAGT TCGGATCACAGACCCAGT TCGGATCACAGACCCAGT TCGGATCACAGACCCAGT TCCGCTGGATCACAGACCCAGT TCCGCTGGATCACAGACCCAGT TCCTCAGCACCAGACCCAGC TTACGCTGCACCAGACCCAGC TTACGCTGCACCAGACCACCAGCA	353	TTCACACGGTCTGCGAGCTT
TCCAGCGTACCTGCTTGTAG TCCAGCGAAGTGATCAGAG TCCAGCGAAGTGATGAGAA TGCAGCGGATCGCCATATA TGCAGCGGATCGCCATATA TGCAGCGGATCAGCGTAT TGCAGCGGATCAGGTAT TGCAGCGGATCAGGTAT TGCAGCGGATCTCAGCGTA TGCAGCAGTTCTCAGCGTA TTATCGCAGTGCTCACTG TTATCGCAGTGCTCAGGCT TTATCGCAGTGCTCAGGCT TTTTCGTAGCTGCGCCTAGT TATTTATACTGCGAGCCCAGCTT TATTTATACTGCGAGCGAGG TATTCGAGCTAGGACGAGA TATTTATACTGCGAGCGAGG TATTGATAGCATGGGACGTT TCGGATAGCATGGGACGTT TCGGATAGCAGTGCCCTAA TCGGATCACCGAGGCCATAA TCGGATCACCGAGGCCATAA TCGGATCACCAGGCCATAA TCGTTGTACCAGGCCATAA TCGTTGTACCAGACCCAGT TACCTGAACGCAGACCCAGT TCCGATTGACCAGACCCAGT TCCGATTGACCAGACCCAGT TCCGATCGCACCAGACCCAGT TCCGACCAGACCCAGACCCAGT TCCGACCAGACCCAGCACACACACACACACACACACACAC	354	CTTCAGACAGGAGGAGATAT
357 CTCCAGTCAAGTGCTTCGAG 358 CTCCAGCGAAGTGATGAGAA 359 TGTCAGCGGATCGCCATATA 360 TCCATGCGAGGATCAGGTAT 361 TGCAAGCAGTTCTCAGCGTA 362 TGTAGGACCTGTGCTCACTG 363 TTTATCGCAGTGCTCAGGCT 364 TATGTCAGCAGGCCCAGCTT 365 TTCTCGTAGCTGGCCCTAGT 366 TATTCGAGCTAGGACGCAT 367 TATTTATACTGCGAGCGAGG 368 GACCTTACACTGGCACGAGA 369 TACTGATAGCATGGGACGTT 370 TCGGATAGCAGGGCCATTA 371 GCTGATGCACGAGGCCATTA 372 GCTGGATCACGAGGCCATTA 373 CGCTTTGTACCAGGCCATAG 374 CGTGATGCACGAGCCATAG 375 TACGCTGGATCAGACCCAGT 376 ATCCTGAACGCAGACCCAGT 377 ATCGTTGCACCAGACCCAGT 378 CTCTCAGGACCAGACACCAG 379 TCTGAGCGATCTGCCAGTCA 380 GGTGAGACCTATGTATATCG 381 TTAGAGTCTTAGGCATGTCG 382 TTATAGCCGTAGGCAGCAC 383 CTCTAAGTATTGGACACGCA 384 GCTAGGATATAGGACACTGA 385 GCTATCGAATGTGCAGTACG	355	TCCAGCCGACGTGCGATTTA
TGTCAGCGAAGTGATGAGAA TGTCAGCGGATCGCCATATA TGCATGCGAGGATCAGGTAT TGCAAGCAGTTCTCAGCGTA TGCAAGCAGTTCTCAGCGTA TGCAAGCAGTTCTCAGCGTA TGTAGGACCTGTGCTCACTG TTATGCAGCAGTGCTCAGGCT TATGTCAGCAGGCCCAGCTT TCTCGTAGCTGCGCCTAGT TATTTATACTGCGAGCGCAGG TATTTATACTGCGAGCGAGG TATTTATACTGCAGCAGGCCAGAGA TATTTATACTGCAGCAGAGA TATTTATACTGCAGCAGAGA TATTTATACTGCAGCACCAGAGA TCTGATAGCATGGGACGCTTA TCGGATAGCAGTGCCCTTA TCGGATAGCAGGCCATTA TCGGATCACCAGAGCCCATTA TCGTGATCACCAGAGCCCATA TACCTTGTACCAGGCCATAG TACCTGAACCAGACCCAGT TACCTGAACCAGACCCAGT TACCTGAACGCAGACCCAGT TCTGAGCGATCAGACCAGAC	356	TCCAGCGTACCTGCTTGTAG
TGTCAGCGGATCGCCATATA TCCATGCGAGGATCAGGTAT TGCAAGCAGTTCTCAGCGTA TGCAAGCAGTTCTCAGCGTA TGTAGGACCTGTGCTCACTG TTATCGCAGTGCTCAGGCT TATGTCAGCAGGCCCAGCTT TTCTCGTAGCTGCGCCTAGT TATTCAGCAGGCCCAGCTT TATTCAGCAGGCCCAGCTT TATTCAGCTAGGCACGCAT TATTCACTGCGACGCAGG TATTCACTGCGACGAGG TATTCACTGCACGAGCAGA TATTTATACTGCGAGCGAGA TACTGATAGCATGGCACGAGA TCGGATAGCATGGCACGTT TCGGATAGCACGAGGCCATTA TCGCTGATCACAGAGCCCATTA TCGCTGATCACAGAGCCCATA TACCTGAACCAGACCCAGT TACCTGAACCAGACCCAGT TACCTGAACCAGACCCAGT TACCTGAACCAGACCCAGT TCGAGCCACCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGCACCAC	357	CTCCAGTCAAGTGCTTCGAG
TCCATGCGAGGATCAGGTAT TGCAAGCAGTTCTCAGCGTA TGTAGGACCTGTGCTCACTG TGTAGGACCTGTGCTCACTG TGTATCGCAGTGCTCAGGCT TATGTCAGCAGGCCCAGCTT TATGTCAGCAGGCCCAGCTT TATTCGAGCTAGGGACGCAT TATTTATACTGCGAGCGAGG TATTTATACTGCGAGCGAGG TATTCGATAGCATGGCACGAGA TACTGATAGCATGGCACGAGA TACTGATAGCATGGCACGAGA TACTGATAGCATGGGACGTT TCGGATAGCAGGGCCATTA TCGGATAGCAGGGCCATTA TCGGATCACGAGGCCATTA TCGTGATCACGAGGCCATTA TCGTGATCACAGGCCATAC TACGCTGGATCACAGACCCAGT TACGCTGGATCACAGACCCAGT TACGCTGGATCACAGACCCAGT TACGCTGGATCAGACCCAGT TACGCTGGATCAGACCCAGT TACGCTGGATCAGACCCAGT TACGCTGGATCAGACCCAGACTACA TCCTCAGGACCAGCATGATA TCTCTCAGGACCAGCATGATA TCTGAGCGATCTGCCAGTCA TTAGAGTCTTAGGCATGTCG TTAGAGTCTTAGGCATGTCG TTAGAGTCTTAGGCATGCCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCACACCAGACCCAGACCCAGACCCAGACCCAGACCCCAGACCCCAGACCCCAGACCCCAGACCCCAGACCCCAGCACCAGCACCAGCACCAGCACCAGACCACC	358	CTCCAGCGAAGTGATGAGAA
TGCAAGCAGTTCTCAGCGTA TGTAGGACCTGTGCTCACTG TGTAGGACCTGTGCTCACTG TTATCGCAGTGCTCAGGCT TATGTCAGCAGGCCCAGCTT TATGTCAGCAGGCCCAGCTT TATGTCAGCAGGCCCAGCTT TATTCGAGCTAGGGACGCAT TATTTATACTGCGAGCGAGG GAGA TACTGATAGCATGGCACGAGA TACTGATAGCATGGCACGAGA TACTGATAGCATGGCACGAGA TACTGATAGCATGGGACGTT TCGGATAGCAGGGCCATTA TCGGATAGCAGGGCCATTA TCGGATCACGAGGCCATTA TCGCTGTACCAGGCCATAC TCGCTGTACCAGGCCATAC TACCTGAACCAGACCCAGT TACCTGAACCAGACCCAGT TACCTGAACCAGACCCAGT TACCTGAACGCAGACCCAGC TCCTCAGGACCAGCACTCAC TCCTCAGGACCAGCACTCACA TCTCAGGACCAGCATGATA TCTGAGCGATCTGCCAGTCA TTAGAGTCTTAGGCATGTCG TTAGAGTCTTAGGCATGTCG TTATAGCCGTAGGCAGGTAC TTATAGCCGTAGGCAGCACCAGA TTATAGCCGTAGGCAGCACCAGA TTATAGCCGTAGGCAGCACCAGACCCAGACCCAGACCCAGACCCAGACCCAGCACCAGACCCAGACCCAGACCCAGACCCAGACCCAGACCCAGCACCAGACCACC	359	TGTCAGCGGATCGCCATATA
TGTAGGACCTGTGCTCACTG 363 TTTATCGCAGTGCTCAGGCT 364 TATGTCAGCAGGCCCAGCTT 365 TTCTCGTAGCTGCGCCTAGT 366 TATTCGAGCTAGGGACGCAT 367 TATTTATACTGCGAGCGAGG 368 GACCTTACACTGGCACGAGA 369 TACTGATAGCATGGGACGTT 370 TCGGATAGCATGGGACGTT 371 GCTGATGCACGAGGCCATTA 372 GCTGATGCACGAGGCCATTA 373 CGCTTTGTACCAGGGCCATA 374 CGTGATTGACCAGAGCCATA 375 TACGCTGGATCACGAGCCATA 376 ATCCTGAACGAGCCATCA 377 ATCGTTGCACCAGACCCAG 377 ATCGTTGCACCAGAACTACA 378 CTCTCAGGACCAGCATGATA 379 TCTGAGCGATCTGCCAGTCA 380 GGTGAGACCTATGTATATCG 381 TTAGAGTCTTAGGCATGTCG 382 TTATAGCCGTAGGCAGCAC 384 GCTAGGATATAGGACACTGA 385 GCTATCGAATGTGCAGTACG	360	TCCATGCGAGGATCAGGTAT
TTTATCGCAGTGCTCAGGCT 364 TATGTCAGCAGGCCCAGCTT 365 TTCTCGTAGCTGCGCCTAGT 366 TATTCGAGCTAGGGACGCAT 367 TATTTATACTGCGAGCGAGG 368 GACCTTACACTGGCACGAGA 369 TACTGATAGCATGGGACGTT 370 TCGGATAGCATGGGACGTT 371 GCTGATGCACGAGGCCATTA 372 GCTGATGCACGAGGCCATTA 373 CGCTTTGTACCAGGCCATAG 374 CGTGATTGACCAGACCCAGT 375 TACGCTGGATCAGACCCAGT 376 ATCCTGAACGCAGAGCCATCA 377 ATCGTTGCACCAGACCCAG 377 ATCGTTGCACCAGACCCAG 378 CTCTCAGGACCAGCATAA 379 TCTGAGCGATCTGCCAGTCA 380 GGTGAGACCTATGTATATCG 381 TTAGAGTCTTAGGCATGTCG 382 TTATAGCCGTAGGCAGCAC 384 GCTAGGATATGGACACCCA 385 GCTATCGAATGTGCAGTACG 386 GCTAGGATATAGGACACTGA 387 CTCTAAGTATTGGACACCCA 388 GCTAGGATATAGGACACTGA 389 GCTATCGAATGTGCAGTACC	361	TGCAAGCAGTTCTCAGCGTA
TATGTCAGCAGGCCCAGCTT 365 TTCTCGTAGCTGCGCCTAGT 366 TATTCGAGCTAGGGACGCAT 367 TATTTATACTGCGAGCGAGG 368 GACCTTACACTGGCACGAGA 369 TACTGATAGCATGGGACGTT 370 TCGGATAGCAGTGCGCTCTA 371 GCTGATGCACGAGGCCATTA 372 GCTGGATCACGAGGCCATTA 373 CGCTTTGTACCAGGCCATAG 374 CGTGATTGACCAGACCCAGT 375 TACGCTGGATCAGACCCAGT 376 ATCCTGAACGCAGAGACACG 377 ATCGTTGCACCAGAGCACACA 378 CTCTCAGGACCAGCATAA 379 TCTGAGCGATCTGCCAGTCA 380 GGTGAGACCTATGTATATCG 381 TTAGAGTCTTAGGCATGTCG 382 TTATAGCCGTAGGCAGGAC 384 GCTAGGATATAGGACACTGA 385 GCTATCGAATGTGCAGTACG 385 GCTATCGAATGTGCAGTACG	362	TGTAGGACCTGTGCTCACTG
TTCTCGTAGCTGCGCCTAGT TATTCGAGCTAGGGACGCAT TATTTATACTGCGAGCGAGG GACCTTACACTGGCACGAGA GACCTTACACTGGCACGAGA TACTGATAGCATGGGACGTT TCGGATAGCATGGGACGTT TCGGATAGCAGTGCGCTCTA TCGGATGCACGAGGCCATTA CCTGATGCACGAGGCCATTA CCTGATTGACCAGAGCCCATA TCGTGATTGACCAGACCCAGT TACGCTGGATCACGAGCCATA TACGCTGGATCAGACCCAGT TACGCTGGATCAGACGGTCA TACGCTGGATCAGACCCAGT TACGCTGGATCAGACCCAGT TCTGAACGCAGAACTACA TCTCAGGACCAGCATGATA TCTGAGCGATCTGCCAGTCA CTTTGAGCGATCTGCCAGTCA TTAGAGTCTTAGGCATGTCG TTATAGCCGTAGGCAGGTAC TTATAGCCGTAGGCAGGTAC TTATAGCCGTAGGCAGCACGA CTCTAAGTATTGGACACCGCA CTCTAAGTATTGGACACCCA CTCTAAGTATTGGACACCCA CTCTAAGTATTGGACACCCA CTCTAAGTATTGGACACCCCA CTCTAAGTATTGCAGTACCG CTCTAAGTATTGCAGTACCG CTCTAAGTATTGCAGTACCG CTCTAAGTATTGCAGTACCG	363	TTTATCGCAGTGCTCAGGCT
366 TATTCGAGCTAGGGACGCAT 367 TATTTATACTGCGAGCGAGG 368 GACCTTACACTGGCACGAGA 369 TACTGATAGCATGGGACGTT 370 TCGGATAGCAGTGCGCTCTA 371 GCTGATGCACGAGGCCATTA 372 GCTGGATCACGAGGCCATTA 373 CGCTTTGTACCAGGCCATAG 374 CGTGATTGACCAGACCCAGT 375 TACGCTGGATCAGACCCAGT 376 ATCCTGAACGCAGACCCAG 377 ATCGTTGCACCAGAACTACA 378 CTCTCAGGACCAGCATGATA 379 TCTGAGCGATCTGCAGTCA 380 GGTGAGACCTATGTATATCG 381 TTAGAGTCTTAGGCATGTCG 382 TTATAGCCGTAGGCAGGTAC 383 CTCTAAGTATTGGACACCCA 384 GCTAGGATATAGGACACTGA 385 GCTATCGAATGTGCAGTACG	364	TATGTCAGCAGGCCCAGCTT
TATTTATACTGCGAGCGAGG GACCTTACACTGGCACGAGA GACCTTACACTGGCACGAGA TACTGATAGCATGGGACGTT TCGGATAGCAGTGCGCTCTA TCGGATGCACGAGGCCATTA CCTGATCACCAGAGCCCATA CGCTTTGTACCAGGCCATAG TACGCTGGATCACAGACCCAGT TACGCTGGATCAGACCCAGT TACGCTGGATCAGACCCAGT ATCCTGAACGCAGACCACA TCGTGACCAGACCA	365	TTCTCGTAGCTGCGCCTAGT
GACCTTACACTGGCACGAGA GACCTTACACTGGCACGAGA GACCTTACACTGGCACGAGA GACCTTACACTGGCACGAGA GACCTTACACTGGCACGACGTT GACTGATGCACGAGGCCATTA GCTGATGCACGAGGCCATTA GCTGATCACCAGGCCATAG GCTGATTGACCAGGCCATAG GCTGATTGACCAGACCCAGT TACGCTGGATCAGACCCAGT ATCCTGAACGCAGAGCACCAG ATCCTGAACGCAGAGCACCAG ATCCTCAGGACCAGCATAA GCTCTCAGGACCAGCATAA GCTCTCAGGACCAGCATAA GCTAGACCCAGTCA GCTAGACCCAGTCA GCTAGACCCAGTCA GCTAGAGCCATGTATATCC GCTAGAGCCATGTCACA GCTAGAGCCATGTCACA GCTAAGTATTGGACACCCA GCTAGGATATAGGACACTGA GCTAGGATATAGGACACTGA GCTAGGATATAGGACACTGA GCTAGGATATAGGACACTGA GCTAGGATATAGGACACTGA GCTATCGAATGTGCAGTACC	366	TATTCGAGCTAGGGACGCAT
TACTGATAGCATGGGACGTT TCGGATAGCAGTGCGCTCTA TCGGATAGCAGTGCGCTCTA TCGGATGCACGAGGCCATTA TCGCTGATCACGAGGCCATTA TCGCTGATCACGAGGCCATAG TCGCTGATTGACCAGGCCATAG TCGCTGATTGACCAGACCCAGT TACGCTGGATCAGACGCAGT TACGCTGGATCAGACGCAGAGCACAG TCCTGAACGCAGAGACACG TCCTCAGGACCAGAACTACA TCCTCAGGACCAGCATGATA TCTGAGCGATCTGCCAGTCA TCTGAGCGATCTGCAGTCA TTAGAGTCTTAGGCATGTCG TTATAGCCGTAGGCAGGTAC TTATAGCCGTAGGCAGGTAC TCCTAAGTATTGGACACCCA TCCTAAGTATTGGACACCCA TCCTAAGTATTGGACACCCA TCCTAAGTATTGGACACCCA TCCTAAGTATTGGACACCCA TCCTAAGTATTGGACACCCA TCCTAAGTATTGGACACCCCA TCCTAAGTATTGGACACCCCA TCCTAAGTATTGGACACCCCA TCCTAAGTATTGGACACCCCA TCCTAAGTATTGGACACCCCA TCCTAAGTATTGGACACCCCA TCCTAAGTATTGCAATCCCCACCCA TCCTAACTATCCCAATCTCCCACTACCCCCA TCCTAACTATCCCAATCTCCCACTACCCCCACCCCACCCCACCCCACCCCACCCCACCCCACCCC	367	TATTTATACTGCGAGCGAGG
TCGGATAGCAGTGCGCTCTA GCTGATGCACGAGGCCATTA GCTGATGCACGAGGCCATTA GCTGATCACGAGGCTCATA GCTGGATCACGAGGCTCATA GCTGATTGACCAGGCCATAG GCTGATTGACCAGACCCAGT ACGCTGGATCAGACGGTCA ACCTGAACGCAGAGACACG ACCTGAACGCAGAACTACA TCGTTGCACCAGAACTACA TCTGAGCGATCTGCCAGTCA GCTGAGACCAGCATGATA TCTGAGCGATCTGCCAGTCA GCTGAGACCTATGTATATCG TTAGAGTCTTAGGCATGTCG TTATAGCCGTAGGCAGGTAC GCTAGGATATTGGACACCCA ACCTAGGATATAGGACACTGA GCTAGGATATAGGACACTGA GCTAGGATATAGGACACTGA GCTATCGAATGTGCAGTACG	368	GACCTTACACTGGCACGAGA
371 GCTGATGCACGAGGCCATTA 372 GCTGGATCACGAGGCCATTA 373 CGCTTTGTACCAGGCCATAG 374 CGTGATTGACCAGACCCAGT 375 TACGCTGGATCAGACGGTCA 376 ATCCTGAACGCAGACCAG 377 ATCGTTGCACCAGAACTACA 378 CTCTCAGGACCAGCATGATA 379 TCTGAGCGATCTGCCAGTCA 380 GGTGAGACCTATGTATATCG 381 TTAGAGTCTTAGGCATGTCG 382 TTATAGCCGTAGGCAGGTAC 383 CTCTAAGTATTGGACACGCA 384 GCTAGGATATAGGACACTGA 385 GCTATCGAATGTGCAGTACG	369	TACTGATAGCATGGGACGTT
372 GCTGGATCACGAGGCTCATA 373 CGCTTTGTACCAGGCCATAG 374 CGTGATTGACCAGACCCAGT 375 TACGCTGGATCAGACGGTCA 376 ATCCTGAACGCAGAGCACG 377 ATCGTTGCACCAGAACTACA 378 CTCTCAGGACCAGCATGATA 379 TCTGAGCGATCTGCCAGTCA 380 GGTGAGACCTATGTATATCG 381 TTAGAGTCTTAGGCATGTCG 382 TTATAGCCGTAGGCAGGTAC 383 CTCTAAGTATTGGACACGCA 384 GCTAGGATATAGGACACTGA 385 GCTATCGAATGTGCAGTACG	370	TCGGATAGCAGTGCGCTCTA
373 CGCTTTGTACCAGGCCATAG 374 CGTGATTGACCAGACCCAGT 375 TACGCTGGATCAGACGGTCA 376 ATCCTGAACGCAGAGACACG 377 ATCGTTGCACCAGAACTACA 378 CTCTCAGGACCAGCATGATA 379 TCTGAGCGATCTGCCAGTCA 380 GGTGAGACCTATGTATATCG 381 TTAGAGTCTTAGGCATGTCG 382 TTATAGCCGTAGGCAGGTAC 383 CTCTAAGTATTGGACACCCA 384 GCTAGGATATAGGACACTGA 385 GCTATCGAATGTGCAGTACG	371	GCTGATGCACGAGGCCATTA
374 CGTGATTGACCAGACCCAGT 375 TACGCTGGATCAGACGGTCA 376 ATCCTGAACGCAGAGACACG 377 ATCGTTGCACCAGAACTACA 378 CTCTCAGGACCAGCATGATA 379 TCTGAGCGATCTGCCAGTCA 380 GGTGAGACCTATGTATATCG 381 TTAGAGTCTTAGGCATGTCG 382 TTATAGCCGTAGGCAGGTAC 383 CTCTAAGTATTGGACACGCA 384 GCTAGGATATAGGACACTGA 385 GCTATCGAATGTGCAGTACG	372	GCTGGATCACGAGGCTCATA
TACGCTGGATCAGACGGTCA ATCCTGAACGCAGAGACACG ATCCTGAACGCAGAGACACG ATCGTTGCACCAGAACTACA ATCGTTGCACCAGAACTACA TCTCAGGACCAGCATGATA TCTGAGCGATCTGCCAGTCA GGTGAGACCTATGTATATCG TTAGAGTCTTAGGCATGTCG AS2 TTATAGCCGTAGGCAGGTAC AS3 CTCTAAGTATTGGACACGCA GCTAGGATATAGGACACTGA GCTAGGATATAGGACACTGA GCTATCGAATGTGCAGTACG	373	CGCTTTGTACCAGGCCATAG
376 ATCCTGAACGCAGAGACACG 377 ATCGTTGCACCAGAACTACA 378 CTCTCAGGACCAGCATGATA 379 TCTGAGCGATCTGCCAGTCA 380 GGTGAGACCTATGTATATCG 381 TTAGAGTCTTAGGCATGTCG 382 TTATAGCCGTAGGCAGGTAC 383 CTCTAAGTATTGGACACGCA 384 GCTAGGATATAGGACACTGA 385 GCTATCGAATGTGCAGTACG	374	CGTGATTGACCAGACCCAGT
377 ATCGTTGCACCAGAACTACA 378 CTCTCAGGACCAGCATGATA 379 TCTGAGCGATCTGCCAGTCA 380 GGTGAGACCTATGTATATCG 381 TTAGAGTCTTAGGCATGTCG 382 TTATAGCCGTAGGCAGGTAC 383 CTCTAAGTATTGGACACGCA 384 GCTAGGATATAGGACACTGA 385 GCTATCGAATGTGCAGTACG	375	TACGCTGGATCAGACGGTCA
378 CTCTCAGGACCAGCATGATA 379 TCTGAGCGATCTGCCAGTCA 380 GGTGAGACCTATGTATATCG 381 TTAGAGTCTTAGGCATGTCG 382 TTATAGCCGTAGGCAGGTAC 383 CTCTAAGTATTGGACACGCA 384 GCTAGGATATAGGACACTGA 385 GCTATCGAATGTGCAGTACG	376	ATCCTGAACGCAGAGACACG
TCTGAGCGATCTGCCAGTCA GGTGAGACCTATGTATATCG TTAGAGTCTTAGGCATGTCG TTATAGCCGTAGGCAGGTAC TTATAGCCGTAGGCAGGTAC CTCTAAGTATTGGACACGCA GCTAGGATATAGGACACTGA GCTATCGAATGTGCAGTACG	377	ATCGTTGCACCAGAACTACA
380 GGTGAGACCTATGTATATCG 381 TTAGAGTCTTAGGCATGTCG 382 TTATAGCCGTAGGCAGGTAC 383 CTCTAAGTATTGGACACGCA 384 GCTAGGATATAGGACACTGA 385 GCTATCGAATGTGCAGTACG	378	CTCTCAGGACCAGCATGATA
TTAGAGTCTTAGGCATGTCG 382 TTATAGCCGTAGGCAGGTAC 383 CTCTAAGTATTGGACACGCA 384 GCTAGGATATAGGACACTGA 385 GCTATCGAATGTGCAGTACG		
TTATAGCCGTAGGCAGGTAC 383 CTCTAAGTATTGGACACGCA 384 GCTAGGATATAGGACACTGA 385 GCTATCGAATGTGCAGTACG	380	GGTGAGACCTATGTATATCG
383 CTCTAAGTATTGGACACGCA 384 GCTAGGATATAGGACACTGA 385 GCTATCGAATGTGCAGTACG		
GCTAGGATATAGGACACTGA GCTATCGAATGTGCAGTACG		TTATAGCCGTAGGCAGGTAC
385 GCTATCGAATGTGCAGTACG		CTCTAAGTATTGGACACGCA
	384	GCTAGGATATAGGACACTGA
386 TCTATCCACTGCGGACGAGT		
		TCTATCCACTGCGGACGAGT
387 TCATACTCATGTGCAGCTCT		
388 TCATCGAGATCGGCCACTGT	388	TCATCGAGATCGGCCACTGT

Seq. Id	3' to 5' sequence
389	CTTATGATACCAGTCAGCAC
390	TATTGGTACGGAGTTAGCCC
391	GTAGATGACCCAGTTCCAGC
392	GGCTGTTACCGAGTCTCAGA
393	TGCTAGTTAGGAGTATCGCA
394	GGCTTACTAGCAGTCACGCA
395	CAGCATATAAGAGTCGTACC
396	GGCATCATAGACGCTACGCT
397	GAGTCAGCAATCGCAGCTAA
398	GATCAGTAATGCGGAGCAAC
399	TATCATAGATGCGGACGGAT
400	CAGTCCACAAGCGCGAGTAA
401	CGTAGCCCAAGTGCCGATAT
402	GACGCACCACAGGCTAGTAT
403	CTAGCATACCAGGCGAGAGT
404	AGTGCATCACAAGAGACTCG
405	GCCATAGACGAGGCAGTATC
406	GGAATACGCTGAGATATACG
407	GTTAATCGCTCAGCAGCATT
408	CACAAGCGACCAGAAGCGTT
409	TCTTATCGACCAGGGCGGTT
410	GACACTATCCCAGACGGAGT
411	TTACTAGGTTCAGCGCGATC
412	TTCAGATCCTCAGCGTAGTC
413	TCTCAGATATTCGTAGCAGC
414	TGTCTATTAGTAGCTGCGAG
415	TAGATACTCTGAGCTAGGAG
416	TGTCTCCAGATCGTGCGAGT
417	TTCGGTCTAGCTGGTAGCAT
418	ATCTGGCGAACAGGTGCATA
419	AATGCGCGAAACGGCGATAC
420	TTTGTCGCAGTAGTCGCATC
421	TGTTGTGCAGTCTCCAGGCA
422	CATTGTGAACTCTACGTCAG
423	CGGATGTCAAGCTCTCACAG
424	CTGCGGCAATACTCTCAGGT
425	ATGCGGAGAACCTCTGACAA
426	GCGCGTGAATCCTGTGACTA
427	GCGCTCTGAATCTGTGAGAA
428	GCGCTATGAATGTCAGCTAA
429	GCCGAGGTAATGTGATATAC
430	GCCGCGTGAATATGAAGATA
431	GCGGCGAGAATCTTCCGATA
432	GATGGTAGAATCTCTCTCAC
433	GCTGCGGGAGACTATCATCT
434	GCTGGATTACGATGCCATAG
435	GTTGATTCACGATGCCATAG
436	CTTCACGCAAGTTGTCCAGA
-50	OTTOROGORAGITATOOAGA

Seq. Id	3' to 5' sequence
437	
	CTTACGCCAAGTTGTCAGAA
438	CTTGCGTCAATAGTCTGAGA
439	CCTGTGCGAACTGTCTTACA
440	CTCAGTCCAAGTGGCTCAGA
441	CCATAGCGAAGCGCACAGTA
442	CCAGCACTAAGCGCAGATAG
443	CTCCGCCTAAGTGGCAGTAA
444	TGCGCCTGACGTTCGGATTA
445	TGTCCAGTAGCTTGAGAGTC
446	GCTCACAGAGTTTGATAGAC
447	GCTACAGGAGTGGATATTAC
448	GTGACAGTGGCAGATATAAC
449	TCGCACTGAGCTGTAATCGA
450	TCTTATGAGATGTAGCTCGC
451	TCCATCTAGCTGTAGCCGAA
452	GTCATAGCAGCTTAGACCTA
453	TTATGCTGACTGTGCTCGAC
454	TTAGTGCAGTATTAGTCGCG
455	TGTCTGACCTTGTAGCCGAC
456	TGTTGACACTTGCGTACCGG
457	TCTTAGCATGTGCGACGACG
458	GCTAAGCTCTTGCACTGACG
459	CATAAGACTTTCCAATCGCG
460	CTGAAGCACTTTCCACGAAG
461	CTGAACCCGTTGCAGAGAGA
462	CGGAACCGATGGCACAATAT
463	GGTGACCGATGGCTACTCAT
464	ATGGCGCGAACCCTGTACTA
465	CATCGCGGAAGCCACGTATA
466	GACGGCAGAATGCAGTATAT
467	CGCGGAAGAAAGCATATTTG
468	CTCAAGGCACGCAATCTAG
469	TCACAGGAGGCTCGACTCTA
470	CGACAAGGCATTCACACTAG
471	ATAAAGGTCATGCCAACCGC
472	TATAATGCGTTTCACGTCCC
473	TCTAATGCCTGACACGAAAC
474	TGAATGCCGTGACTCGTAAA
475	GTGGAGGCACTGCATCATAA
476	GTGGTGTGACCTCGCCATTA
477	GGAGATGCACTACGGACTAT
478	GAGGATCGAATACTGTCGTA
479	CGGAGAGCAAGTCATACGAC
480	GCAGGAGACGGACTATACTA
481	GAGCGTGTAATCCGATCTAA
482	CGATACGGAAGGCGCACTAA
483	CGATAGGTAAGGCGACTCAA
484	GATGTGGCACGACGATCATA

TGAGTAGGCAGTCCGATCTA 486 TGATAGGCAGTGAGTTCATC 487 TTATGGCGAGAGTTGTCATC 488 GTTTAGGCACGATGCTGTAT 489 GCGTTAGGACCATAGTCTAC 490 CCGATGCGACAATACGTTAG 491 TCTAGCGTCCCATAGCGTAG 492 CTGCTTGGACCATAGCAGCA 493 CTGCTTGCACGATGAGCGAA 494 TAGCCCGGACGATGTAGTCA 495 CCGCTACAAGCATGAGCAA 496 CGGCTAGAAGAATGATCA 497 CCGATGATAAGCTAGC 498 GCGATGAAACAGCA 499 GCCACTAGACCATAGTAGC 499 GCCACTAGACCATCGGTAT 500 GCACGCGGACCATCGTTAT 501 GCCGCTCGACCATAGTGATA 502 GCCGAGTCACCATAGTGATA 503 CACGGGTCACCATAGTGATA 504 GACGCCGACCATAGTGATA 505 TGTGCGTCAGCAGTTATT 506 GCTCGGCTCACCAGTTATT 507 CGCTGGACCATGTTAT 508 CGGTGGACACCATGTTAT 509 CGCGGGACCACCATGTAT 509 CGCGGGACCACAGTTATA 510 GCTCGCGCATTAGCA 511 GCTGCCCATTAGCATA 512 CGCTGACCATAGCATTAA 513 ACGCACCACGCATTAGA 514 CACAGACCACCAGCATTAG 515 CCTAGCCCAAGCGATTAG 516 CCGTAGCCCAAGCATTAGA 517 CAGTGCGCCAAGCATTAGA 518 GAGCCACCACGATTAGA 519 GGTCACCACAGCATTAGA 510 GGTGCACCACCACGATTAGA 511 GCTGCCCAAGCCATTAGA 512 CGCTGACCCACGCATTAGA 513 ACGCACCACCAGCATTAA 514 CACAGACCACAGCATTAGA 515 CCTAGCCCAAGGCATTAGA 516 CCGTAGCTCAAGCCATTAGA 517 CAGTGCGCCAAGGCATTAGA 518 GAGCCACCACCACGATTAGA 519 GGTCACCACCACGATTAGA 519 GGTCACCACCACGATTAGA 519 GGTCACCACCACAGCATTAGA 510 GGTGCCCAAGGCATTAGA 511 GCGTAGCCCAAGGCATTAGA 512 CGCTGACCCACAGCATTAGA 513 ACGCACCACAAGCTATGA 514 CACAGACCACAAGCTATGA 515 CCTAGCCCAAGGCATTAGA 516 CCGTAGCTCAAGGCATTAGA 517 CAGTGCGCCAAGGCATTAGA 518 GAGCCACCACAGGCATTAGA 519 GGTCACCACTCAGCGATTAT 520 GTGTCCCCACGAGTCATTA 521 GGAGACCCACAGAGCATATT 522 CGCTGTAAGGATGCCAATATT 522 CGCTGTAAGGATGCCAATATT 523 GTCGTCCACCAGATCCACAATAT 524 GTTCCGCACGATGCCAAAT 525 GCTGCACCACTCATGCCAATAT 526 GTTCCGCACGATCATCACCAATATCCCAATACCAACAACAACAACAACAA	Seq. Id	3' to 5' sequence
486 TGATAGGCAGTGAGTTCATC 487 TTATGGCGAGAGTTGTCATC 488 GTTTAGGCACGATGCTGTAT 489 GCGTTAGGACCATAGTCTAC 490 CCGATGCGACAATACGTTAG 491 TCTAGCGTCCCATAGCGTAG 492 CTGTCTGGACCATAGCAGCA 493 CTGCTTGCACGATGAGCAA 494 TAGCCCGGACGATGAGCAA 495 CCGCTACAAGCATTAGGAAT 496 CGGCTAGAAGAATAGATCA 497 CCGATGATAAGCTAGTAGC 498 GCGGTAGAAGAATAGTCA 499 GCCACTAGACCATCGTTAT 500 GCACGCGGACCATCGTTAT 501 GCCGCTCGACCATAGTGAT 502 GCCGAGTCACCATGCTAT 503 CACGGGTCACCATGCTTAT 504 GACGGCGACCATGGTAT 505 TGTGCGTCAGCAGTTAGTAT 506 GCTCGGCTACCAGCGTTAT 507 CGCTGGACCACTGGTAT 508 CGCTGGACCACATGTATA 509 CGCGGGACCCAGGTTATAT 509 CGCGGGACCCAGCTATTA 509 CGCGGGACCCAGCATATAA 510 GCTCGCGCATTAGCAT 511 GCTGCGCATTAGCATACA 512 CGCTGACCATCACAGCATTAGA 513 ACGCAACCACACGCATTAGA 514 CACAGACCACACGCATTAG 515 CCTAGCCCAAGCATTAGA 516 CCGTGATCCACCGCATTAGA 517 CAGTGCGCCAAGCATTAG 518 GAGCCACCACAGCATATA 519 GGTCACCACAGCATTATA 519 GGTCACCACAGCATTATA 519 GGTCACCACAGCATATA 519 GGTCACCACAGCATTATA 519 GGTCACCACAGCATATA 519 GGTCACCACAGCATATA 519 GGTCACCACAGCATATA 519 GGTCACCACAGCATATA 519 GGTCACCACACAGCATATA 519 GGTCACCACTCAGCCATTT 521 GGAGACCCACTAGGCATATT 522 CGCTGTAAGGATGCCAATT 523 GTCGCCCAAGGCATATT 524 GTTCCGCACGATGCCAATT 525 GCTGCACCACACACCACATT 526 GTTCACCACGATGCCAAT 527 CTCTACGAATCATGCCGAAG		
487 TTATGGCGAGAGTTGTCATC 488 GTTTAGGCACGATGCTGTAT 489 GCGTTAGGACCATAGTCTAC 490 CCGATGCGACAATACGTTAG 491 TCTAGCGTCCCATAGCGTAG 492 CTGTCTGGACCATAGCAGCA 493 CTGCTTGCACGATGAGCGAA 494 TAGCCCGGACGATGTAGTCA 495 CCGCTACAAGCATTGGGAAT 496 CGGCTAGAAGAATGATGCT 497 CCGATGATAAGCTAGTAGC 498 GCGGATAAGCCATATTGAC 499 GCCACTAGACCATTATTGAC 499 GCCACTAGACCATCGTTAT 500 GCACGCGGACCATAGTGAT 501 GCCGCTCGACCATAGTGAT 502 GCCGAGTCACCATGCTGTAT 503 CACGGGTCACCATGCTGTAT 504 GACGGCGACCCAGGTTATAT 505 TGTGCGTCAGCAGTCGTTAT 506 GCTCGGCTACCAGCGTATT 507 CGCTGGACACCATGTGATA 508 CGGTGGACACCACGTTATA 509 CGCGGGACACCACGCATATA 509 CGCGGGACACCACGCATATA 510 GCTCGCCATTAGCATATA 511 GCTGACATCCACGCATTAGA 512 CGCTGACCACAGCATTAGA 513 ACGCAACCACAGCATTAG 514 CACAGACCACAGCATTAG 515 CCTAGCCCAAGCCATTAGA 516 CCGTACCCACAGCATTAGA 517 CACAGCCCAAGCATTAGA 518 GACCACCACAGCATTAA 519 GGTCACCACAGCATGTA 519 GGTCACCACAGCATGTA 519 GGTCACCACAGCATGTA 520 GTGGCCCCAGGCATTAT 521 GGAGACCACAGCATGTA 522 GGTGGCACCACAGCCATATT 523 GTCACCACACAGCCATATT 524 GTTCCGCACGATGCCAATT 525 GCTGCACCACGCATATT 526 GTTCCGCACGATGCCAAT 527 CTCTACGAATCATGCCGAAG	486	
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TGTGCGTCAGCAGTTAGTAT 506 GCTCGGCTACCAGTCGTTAT 507 CGCTGGACACCACTGTGATA 508 CGGTGGAGACCAGATTATAT 509 CGCGGGACACCAGCATATTA 510 GCTCGCGCATTAGCATATAA 511 GCTGACATCCACGCATTGAG 512 CGCTGATCCACCGAGATTAG 513 ACGCAACCAACAGCGAGTGT 514 CACAGACCACAGCATTAGA 515 CCTAGCCCAAGGCATTAGAA 516 CCGTAGCTCCAAGGCATTAGA 517 CAGTGCGCCAGAGCATTA 518 GAGCCACCACGAGTCATA 519 GGTCACCACTCAGCGATGTA 520 GTGTGCCACTCAGCGATTT 521 GGAGACCCGTAGGCATATT 522 CGCTGTAAGGATGCCATATT 523 GTCGTGCAGGATGCCATATT 524 GTTCCGCACGATGCCAGATA 525 GCTGCGACCATCGTCAGTA 526 GTCTAGCGATCATGCCAAT 527 CTCTACGAATCATGCGGAAG		GACGGCGACCCAGGTTATAT
GCTCGGCTACCAGTCGTTAT 507 CGCTGGACACCACTGTGATA 508 CGGTGGAGACCAGATTATAT 509 CGCGGGACACCAGCATATTA 510 GCTCGCGCATTAGCATATAA 511 GCTGACATCCACGCATTGAG 512 CGCTGATCCACCGAGATTAG 513 ACGCAACCACAGCGAGTGT 514 CACAGACCACAAGCTATGGG 515 CCTAGCCCAAGGCATTAGAA 516 CCGTAGCTCCAAGGCATGTA 517 CAGTGCGCCAGAGCATGTA 518 GAGCCACCACGAGTCATGTA 519 GGTCACCACTCAGCGATGTA 520 GTGTGCCACTCAGCGATGTA 521 GGAGACCCGTAGGCATATT 522 CGCTGTAAGGATGCCATATT 523 GTCGTGCAGGATGCCATATT 524 GTTCCGCACGATGCCAGATT 525 GCTGCGACCATCGTCAGATA 526 GTCTAGCGATCATGCCAAT 527 CTCTACGAATCATGCGGAAG	505	
CGCTGGACACCACTGTGATA CGGTGGACACCACTGTGATA CGGTGGAGACCAGATTATAT CGCGGGACACCAGCATATTA CGCGGGACACCAGCATATTA CGCTGCGCATTAGCATATAA CGCTGCGCATTAGCATTAGA CGCTGATCCACCGCATTGAG CGCTGATCCACCGAGATTAG ACGCAACCACACAGCGAGTGT CACAGACCACAAGCTATGGG CCTAGCCCAAGGCATTAGAA CCGTAGCTCCAAGGCATGTA CAGTGCGCCAGAGCAAGTAA CAGTGCGCCAGAGCATGTA CAGTGCGCCACGAGTCATGTA CAGTGCCCACTCAGCGATGTA CGCTAGCCCACTCAGCGATGTA CGCTGCCACTCAGCCATTT CCCCCACGAGCCATATT CCCCCACGAGTCCATATT CCCCCACGAGTCCCAGATT CCCCCACGATGCCACTATT CCCCCCACGATGCCAGATT CCCCCCACGATGCCAGATT CCCCCCCACGATGCCAGATT CCCCCCCACGATCCCAGATA CCCCCCCCCC	506	
CGGTGGAGACCAGATTATAT CGCGGGACACCAGCATATTA CGCGGGACACCAGCATATTA CGCTCGCGCATTAGCATATAA CGCTGACATCCACGCATTGAG CGCTGATCCACCGAGATTAG CGCTGATCCACCGAGATTAG CGCAACCAACAGCGAGTGT CACAGACCACAAGCTATGGG CCTAGCCCAAGGCATTAGAA CCGTAGCTCCAAGGCATGTA CAGTGCGCCAGAGCAAGTAA CAGTGCGCCAGAGCATGTA CAGTGCGCCAGAGCATGTA CAGTGCGCCAGAGCATGTA CGCTAGCCCACTCAGCGATGTA CGCTGCCACTAGGCCGATTT CCCCCACTAGGCCGATTT CCCCCACTAGGCCATATT CCCCCACGAGTCCATATT CCCCCACGATGCCATATT CCCCCACGATGCCAGATA CCCCCACGATGCCAGATA CCCCCCACGATGCCAGATA CCCCCCACGATGCCAGATATT CCCCCCACGATGCCAGATA CCCCCCACGATGCCAGATA CCCCCCCACGATGCCAGATA CCCCCCCACGATGCCAGATA CCCCCCCCACGATCCCCACATCCCCACATCCCCACATCCCCACATCCCCACATCCCCACATCCCCACATCCCCACATCCCCCACATCCCCCACATCCCCCACATCCCCCACATCCCCCACATCCCCCACATCCCCCACATCCCCCACATCCCCCACATCCCCCACATCCCCCC		
CGCGGGACACCAGCATATTA 510 GCTCGCGCATTAGCATATAA 511 GCTGACATCCACGCATTGAG 512 CGCTGATCCACCGAGATTAG 513 ACGCAACCAACAGCGAGTGT 514 CACAGACCACAAGCTATGGG 515 CCTAGCCCAAGGCATTAGAA 516 CCGTAGCTCCAAGGCATGTA 517 CAGTGCGCCAGAGCAAGTAA 518 GAGCCACCACGAGTCATGTA 519 GGTCACCACTCAGCGATGTA 520 GTGTGCCACTAGGCCGATTT 521 GGAGACCCGTAGGCATATT 522 CGCTGTAAGGATGCCATATT 523 GTCGTGCAGGATGCCATATT 524 GTTCCGCACGATGCCAGATT 525 GCTGCGACCATCGTCAGATA 526 GTCTAGCGATCATGCCAAT 527 CTCTACGAATCATGCGGAAG	508	
GCTCGCGCATTAGCATATAA 511 GCTGACATCCACGCATTGAG 512 CGCTGATCCACCGAGATTAG 513 ACGCAACCAACAGCGAGTGT 514 CACAGACCACAAGCTATGGG 515 CCTAGCCCAAGGCATTAGAA 516 CCGTAGCTCCAAGGCATGTA 517 CAGTGCGCCAGAGCAAGTAA 518 GAGCCACCACGAGTCATGTA 519 GGTCACCACTCAGCGATGTA 520 GTGTGCCACTAGGCCGATTT 521 GGAGACCCGTAGGCATAATT 522 CGCTGTAAGGATGCCATATT 523 GTCGTGCAGGATGCCATATT 524 GTTCCGCACGATGCCAGATT 525 GCTGCGACCATCGTCAGATA 526 GTCTAGCGATCATGCTCAAT 527 CTCTACGAATCATGCGGAAG	509	
512 CGCTGATCCACCGAGATTAG 513 ACGCAACCAACAGCGAGTGT 514 CACAGACCACAAGCTATGGG 515 CCTAGCCCAAGGCATTAGAA 516 CCGTAGCTCCAAGGCATGTA 517 CAGTGCGCCAGAGCAAGTAA 518 GAGCCACCACGAGTCATGTA 519 GGTCACCACTCAGCGATGTA 520 GTGTGCCACTAGGCCATGTA 521 GGAGACCCGTAGGCCATATT 522 CGCTGTAAGGATGCTGAATA 523 GTCGTGCAGGATGCCATATT 524 GTTCCGCACGATGCCAGATT 525 GCTGCGACCATCGTCAGATA 526 GTCTAGCGATCATGCTCAAT 527 CTCTACGAATCATGCGGAAG	510	GCTCGCGCATTAGCATATAA
ACGCAACCAACAGCGAGTGT CACAGACCACAAGCTATGGG CCTAGCCCAAGGCATTAGAA CCGTAGCTCCAAGGCATGTA CAGTGCGCCAGAGCAAGTAA CAGTGCGCCAGAGCAAGTAA GAGCCACCACGAGTCATGTA GAGTCACCACTCAGCGATGTA GAGTGCCACTAGGCCGATGTA CAGTGCCACTAGGCCGATGTA CAGTGCCACTAGGCCGATGTA CAGTGCCACTAGGCCGATGTA CAGTGCCACTAGGCCGATGTA CAGTGCCACTAGGCCGATTT CAGTGCCACTAGGCCGATGTA CAGTGCCACTAGGCCATATT CAGTGCCACGATGCCAGATA CAGTGCCACGATGCCAGATA CAGTGCCACCACTAGTCCAGATA CACTGCCACCACTAGTCAAT CACTGCCACCATCATCAAT CACTGCCACCAATCATCCCAAT CACTGCCACCAATCATCAAT CACTGCCACCAATCATCCCAAT CACTGCCACCAATCATCCCAAT CACTGCCACCAATCATCCCAAT CACTGCCACCAATCATCCCAAT CACTGCCACCAATCATCCCAAT CACTGCCACCAATCATCCCCAAT CACTGCCACCAATCATCATCCCCAAT CACTGCCACCAATCATCCCCAAT CACTGCCACCACCACCACCACCAATCATCCCCAAT CACTGCCACCACCACCACCACCACACATCATCCCCAAT CACTGCCACCACCACCACCACCACCACACATCATCCCCAAT CACTGCCACAATCATCAATCATCCCCAATCATCCCCAAT CACTGCCACAATCATCATCAATCATCCCCAATCATCCCCAATCATC	511	GCTGACATCCACGCATTGAG
514 CACAGACCACAAGCTATGGG 515 CCTAGCCCAAGGCATTAGAA 516 CCGTAGCTCCAAGGCATGTA 517 CAGTGCGCCAGAGCAAGTAA 518 GAGCCACCACGAGTCATGTA 519 GGTCACCACTCAGCGATGTA 520 GTGTGCCACTAGGCCGATTT 521 GGAGACCCGTAGGCATAATT 522 CGCTGTAAGGATGCTGAATA 523 GTCGTGCAGGATGCCATATT 524 GTTCCGCACGATGCCAGATT 525 GCTGCGACCATCGTCAGATA 526 GTCTAGCGATCATCGTCAAT 527 CTCTACGAATCATGCGGAAG	512	CGCTGATCCACCGAGATTAG
515 CCTAGCCCAAGGCATTAGAA 516 CCGTAGCTCCAAGGCATGTA 517 CAGTGCGCCAGAGCAAGTAA 518 GAGCCACCACGAGTCATGTA 519 GGTCACCACTCAGCGATGTA 520 GTGTGCCACTAGGCCGATTT 521 GGAGACCCGTAGGCATAATT 522 CGCTGTAAGGATGCTGAATA 523 GTCGTGCAGGATGCCATATT 524 GTTCCGCACGATGCCAGATT 525 GCTGCGACCATCGTCAGATA 526 GTCTAGCGATCATGCTCAAT 527 CTCTACGAATCATGCGGAAG	513	ACGCAACCAACAGCGAGTGT
516 CCGTAGCTCCAAGGCATGTA 517 CAGTGCGCCAGAGCAAGTAA 518 GAGCCACCACGAGTCATGTA 519 GGTCACCACTCAGCGATGTA 520 GTGTGCCACTAGGCCGATTT 521 GGAGACCCGTAGGCATAATT 522 CGCTGTAAGGATGCTGAATA 523 GTCGTGCAGGATGCCATATT 524 GTTCCGCACGATGCCAGATT 525 GCTGCGACCATCGTCAGATA 526 GTCTAGCGATCATGCTCAAT 527 CTCTACGAATCATGCGGAAG	514	CACAGACCACAAGCTATGGG
517 CAGTGCGCCAGAGCAAGTAA 518 GAGCCACCACGAGTCATGTA 519 GGTCACCACTCAGCGATGTA 520 GTGTGCCACTAGGCCGATTT 521 GGAGACCCGTAGGCATAATT 522 CGCTGTAAGGATGCTGAATA 523 GTCGTGCAGGATGCCATATT 524 GTTCCGCACGATGCCAGATT 525 GCTGCGACCATCGTCAGATA 526 GTCTAGCGATCATGCTCAAT 527 CTCTACGAATCATGCGGAAG	515	CCTAGCCCAAGGCATTAGAA
GAGCCACCACGAGTCATGTA GGTCACCACCACGAGTCATGTA GGTCACCACTCAGCGATGTA GGTGTGCCACTAGGCCGATTT GGAGACCCGTAGGCATAATT GCCCCGTAAGGATGCTGAATA GCCCGCACGATGCCATATT GCCCCCCACGATGCCAGATT GCCCGCACGATGCCAGATT GCCCGCACCATCGTCAGATA GCCCGCACGATCATCAGATA GCCCCCCCCCC	516	CCGTAGCTCCAAGGCATGTA
GGTCACCACTCAGCGATGTA GGTGTGCCACTAGGCCGATTT GCAGACCCGTAGGCATAATT GCAGACCCGTAGGCATAATT GCAGACCCGTAGGCATAATA GCAGACCCGTAGGCATAATA GCAGACCATGCCAATATT GCAGACCATCGTCAGATA GCAGACCATCGTCAGATA GCAGACCATCGTCAAT GCAGACCATCATCCAAT CCACCACAATCATCCGGAAG	517	CAGTGCGCCAGAGCAAGTAA
GTGTGCCACTAGGCCGATTT GGAGACCCGTAGGCATATT GE2 CGCTGTAAGGATGCTGAATA GE3 GTCGTGCAGGATGCCATATT GE4 GTTCCGCACGATGCCAGATT GE52 GCTGCGACCATCGTCAGATA GE52 GTCTAGCGATCATGCTCAAT GE52 CTCTACGAATCATGCGGAAG	518	GAGCCACCACGAGTCATGTA
GGAGACCCGTAGGCATAATT 522 CGCTGTAAGGATGCTGAATA 523 GTCGTGCAGGATGCCATATT 524 GTTCCGCACGATGCCAGATT 525 GCTGCGACCATCGTCAGATA 526 GTCTAGCGATCATGCTCAAT 527 CTCTACGAATCATGCGGAAG	519	GGTCACCACTCAGCGATGTA
522 CGCTGTAAGGATGCTGAATA 523 GTCGTGCAGGATGCCATATT 524 GTTCCGCACGATGCCAGATT 525 GCTGCGACCATCGTCAGATA 526 GTCTAGCGATCATGCTCAAT 527 CTCTACGAATCATGCGGAAG	520	GTGTGCCACTAGGCCGATTT
GTCGTGCAGGATGCCATATT 524 GTTCCGCACGATGCCAGATT 525 GCTGCGACCATCGTCAGATA 526 GTCTAGCGATCATGCTCAAT 527 CTCTACGAATCATGCGGAAG	521	GGAGACCCGTAGGCATAATT
524 GTTCCGCACGATGCCAGATT 525 GCTGCGACCATCGTCAGATA 526 GTCTAGCGATCATGCTCAAT 527 CTCTACGAATCATGCGGAAG	522	CGCTGTAAGGATGCTGAATA
525 GCTGCGACCATCGTCAGATA 526 GTCTAGCGATCATGCTCAAT 527 CTCTACGAATCATGCGGAAG	523	GTCGTGCAGGATGCCATATT
526 GTCTAGCGATCATGCTCAAT 527 CTCTACGAATCATGCGGAAG	524	GTTCCGCACGATGCCAGATT
527 CTCTACGAATCATGCGGAAG	525	GCTGCGACCATCGTCAGATA
	526	GTCTAGCGATCATGCTCAAT
528 CTTAGATACTACGAGCACGA	527	CTCTACGAATCATGCGGAAG
	528	CTTAGATACTACGAGCACGA
529 GTGACGCTACGTGAGCCTAA	529	GTGACGCTACGTGAGCCTAA
530 TACCGTGTACGTGAGCGCAT	530	TACCGTGTACGTGAGCGCAT
TACTGCGACGTAGCGAGTCA	531	TACTGCGACGTAGCGAGTCA
TACTAGGTACTCGCGGCACT	532	TACTAGGTACTCGCGGCACT

Seq. Id	3' to 5' sequence
533	TACTGCGTACTCGGAGCATA
534	GCTCACGTACTCGACAGAAA
535	GTGTACTATGTAGCGAGATC
536	TAGTAGTACGCTGTCAGAGC
537	TGTCGTCGAGTCGTAGATAC
538	GTAGTACACGGAGTGATCCT
539	GTAGTACGAGCTGAGACTCT
540	GTGACTAGCTCGTAATTCTG
541	GAGACACGGTACTAGAGACT
542	CAACAGCGTCACAGACATGG
543	CTATGAGACCACCTCGATAT
544	ATTCGGCGACAACGCATTTA
545	GTTGCCGTACTAGGGATACT
546	GGCGCAGTACGATTGACTAT
547	GTGCGACGAGCTTGTCACTA
548	TGCGTGTGACTATTGATACG
549	CGTCTGCGAACTTTGCTACG
550	CTGTAGCGAAGTTCTCATAC
551	TCGGCGTTACGTGCTGACTA
552	TGAGCTATACTCGTCGTCAG
553	CCGATACTAAGCGTTACGAA
554	CGTCATACATAGGACTAGCA
555	CGCACGCTACAGACTATTAT
556	GCGAGCGTACTATACATAAC
557	GCGAGTCTACGACCTCTATA
558	CGGTACGCACGACAGTCATA
559	CGGTACATACGACTATACAG
560	CGCTAGATACACCACTGATA
561	CTCTAGGTACACTACTGCAT
562	CGTCAGAGACACTGGAATAG
563	CTGCGCGTACACTCGGATAT
564	CTGTCGCTACACTCGTGAGA
565	GTAGACGCCTAGTCAGATAG
566	GAGCGACTACGAGCCACTAT
567	GTGCGACTACGTGCATCACT
568	CGTAGGACACGAGCGTATAT
569	GGCGACGACGTGACTATACT
570	CGGTCACGACGACGAGATAT
570 571	GCGTCACGACGACGATATT
572	GTCGCTCACGATGCGGATATT
573 574	GACCGACAGATCACCTCAC
574 575	GACCACCTACATCATATTCT
575 576	GGCGACGTAGATGCCATATCC
576 	GAGACTGTAATCGCATATCC
577	GACTATGTAATCGAGCCTAC
578	GATAGTCGAATCGCGGATAA
579	TATACGGACTGCGCCCTAGA
580	TAGTCTAGCTGAGCCATCGA

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Seq. Id	3' to 5' sequence
581	GTATATGACCTAGTGCCACG
582	GTGTTGTACGATGTGCTCCA
583	GAGTCTGACATAGGGCACCT
584	GAGTTGCACGTAGACGATAC
585	GACTCGCGCATAGACACATG
586	GACAGGCTACGAGACTAGAT
587	GTGACGGCACTAGCAATATA
588	CTGCTCTGACACGCGAGTAT
589	CGGCTGTGACACGAGCTATT
590	CTGGTGCGACACGCCTATAT
591	GTCAGTGGACTAGCCCTACA
592	ATCGAGTCAACCGGCCTAGA
593	TCGATAGCCTACGTGCCGTT
594	GGAGACCTCTACGCACTGTT
595	GCGTGACAGCTCGCACTATA
596	GCGTAGCTCAGCGACATTAA
597	GCTATACGCACCGTCATGTA
598	CGCATACACTCAGCAGAGAT
599	CTACTTACAGCAGCGACGAG
600	ATCTCGACACAAGCTAATCG
601	CATCGGATACACGCATACAG
602	ACATACAACACCGCTTAGGG
603	TACTGAGTCCACGCTCGGTA
604	GATACAGCCTACGACCGGAT
605	GATACATTACTCGACACGCG
606	CGCTACAGAGATGCACAGAG
607	CCGACTGTAACTGCGATGAA
608	GGTGTTATACGTGCATAGCC
609	CTCGTATTAAGTGCGCTACC
610	TATAGTATCGAGGAGCGACC
611	GTATAGTACGTGATAGGCTC
612	GTACGATACGTGACTAGAGC
613	GTAGGTCGAGCTGCATACTC
614	TTACAGTAGTCTGCATCCCT
615	CTAGTCAAGTCTGCATACAG
616	CTGTCTAATACGGCCACATA
617	CTCGCAATACGTGTACCGTG
618	TCCGATCTACGTGACGGTGA
619	TCTCGCCGACGTGGTCTTAA
620	TCTGTCCACGTCGCGGTTAT
621	TCGTCCTGACTCGCTGGTAA
622	GTCCCTAGACTCGCAGTGAT
623	GCGACAGTAGCTGCAATGAT
624	GACGTAATATCGCCACATCA
625	GACGAGGTACAGCGCATACA
	GCAGGTCTACGACGCATACA
626 627	GCAGAGTACGACGCATGAT
627	
628	GAGTAGATACAGGTCACGAT

Seq. Id	3' to 5' sequence
629	GAGCGATCACACGTCCGATT
630	GGTCGCATAGACGTATCAGT
631	GGTGTCTCACGAGTATCGAC
632	GTAGGCTAGACGGTCCACTA
633	GACGGACACTGAGCACATAG
634	GACACCTATGTAGCAATGAC
635	CACAGTACAATAGCACCTGG
636	CACCAGAACGTAGGCACAGT
637	CACTACTCAAGAGCCAGTTA
638	CGCCGACGAATAGCCAGATA
639	GCCGCACTACTAGCGATGAA
640	GACCAGTTACGAGCAGCGAA
641	GATCACGTAGGAGCACCGTA
642	GTACGCAGAGGAGTCATCCA
643	GTCGCTGACTAGGATCACGT
644	TACGCAGACTCGGACTCGAT
645	GTCGCTATATCGGACCTAAC
646	ACTCGCATAAACGACAGTCT
647	TGGAGTCGAGTAGTACATAC
648	TACGACATGGTAGGACGCTA
649	TGACTTCTACGTGGCGATAT
650	TACGCTCCGAGAGGCGATTT
651	CACCTTCGACGAGCAAGAGT
652	TACGCTCGCTCAGCTTAGGT
653	TACGGCATCGACGCTATTGC
654	TACGGCGACTGAGATGCCAT
655	TACGTGCTAGGAGATGTAAC
656	TATCGTCTATCAGATTGCCC
657	TATCGTATCCACGTTCCGAG
658	GATCGTACATCAGTGTCCAC
659	GAGTCTATATCAGTAGCGAC
660	GTTAGTCGATCAGTAGAGCA
661	GTCCTACGATGAGTGACGCA
662	CGTCTTCTAAGCGTGCTGAA
663	GTCTCCTACCGTGAGCAGTA
664	ATCTCACTACAAGAGCCTAG
665	CTGTGACGACCAGACGCTTA
666	CTGAGCGTAAGTGATTGTAC
667	CTCGTAGCAATAGATTTCCC
668	CTACGTGCAATAGCAGCTCA
669	CCGCAGTACAGATAAGTCA
670	CGCCGGATACAGATAAGTCA
671	CTCAGCATACAGAGTACTOG
672	CCGAGCTTACAACGTGTGCA
673	GACGCATTACCACTGGCGAT
674	CAGGGTGTACCACTGGCGAT
675	CGGTGTTTACAGCAATCCAT
676	CTGGCTGCAATAGCGCGATA
0/0	O TOGOTGOANTAGOGOGATA

Seq. Id	3' to 5' sequence
677	TGGGCTACAGTTGCGCTCAT
678	TCTGGCATAGCAGGTGTCAC
679	GGGATTCTACCAGTTCGCAC
680	GAGGATGCAATCGTAGTCAA
681	AGGGATAACCATGCACACCG
682	CATGAAGACTTTGCACTACC
683	CGCCGACCAATGGGCATATA
684	CCCGAGCCAACTGGAGATAA
685	CCCGCAGCAACTGGGATTAA
686	GCCATAGGAGCAGCGATTTA
687	CCGCTTGCAGCAGACGATAT
688	CCGTTTGCAGACAGCCAGTA
689	CCGTTTACAATGAGCACACA
690	CGTTCTTTAATGAGCGACAG
691	CGAGCCTTAATGACGCACAA
692	GGCAGCATACTCACGATCAT
693	CTGCGAGCAATCAGCCGATA
694	CCGCAGCAAGCTATCGAGAA
695	CGGCGTTCAAGCAAACCGAA
696	CAGTTTACAAGCATATCCCG
697	CATTGACGAAGCATAGTTCC
698	CATAGTGCAAGCAGCGACAC
699	ATCTGTGCAACCATAGTACC
700	ACTTGAAATGAGAAGCCCGT
701	CAGGAGAAGCGAATAGCCTC
702	CCAGAGAGAGCAATATCCGC
	CAAGGAATATACAGGCCCGC
704	CAGAACTGAATTACAGCGCC
705	CATCAGACAATTACAGCTCG
706	CACCCGATAAGAGCATACGG
707	CACTCCAGAAGCACGATAGG
708	CAGCACCGAAGCAGAAGTCT
	CAGATCAGAAGCAGGACGCT
710	CAGACCATAAGCACAGGCGT
711	ACAACACAAATGGCGCGGCT
	ACGCAGATAAATCACCTCGG
	CAAGACAGAATACTCTCCGG
	CACAATACAATAGGCTCGCG
	CAATAAGACATAGGCCGCCG
	CACAACGGATTAGAAGCGCG
	GACATGATATGAGAATGCGC
	AGCAAACTAAGAGCCGGGTC
	AACAATACAACCGTCGGCGG
	AAATAACTAACCGCCTGCGT
	CAAACACGAAGAGCCTGTCG
	CACTAATCAAGCGACAGGCG
	CATATACCAAGCTATCAGCG
724	CACATTCAAGACGATCACGT

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Seq. Id	3' to 5' sequence
725	CACCTATGAAGAGACTCACG
726	AACTATATCAAAGCCCTGGC
727	ACAATACCAAATGCGCCGGG
728	AGAAACGCAAATGCCTCTCG
729	CGAAAGCATAATAGCGGTGC
730	GGCAGAATCTCGTGTACTAG
731	GGTACATTATGCTAGAGAGC
732	GATACATGATGATAGCAGCG
733	AGAACAGGAACATCGCTGCC
734	AGATAAGCAACATCCTGTCC
735	CATAAGCTAAGATCCTGGAC
736	ATTTAGCGAAGAAGCATGGC
737	ATAGCTCAATCAACGATGCG
738	TATATCGCATCCACTCTGGG
739	CATCTCCGAAGCACATTGAG
740	CATTCGTCAAGCACTTCAGA
741	CATTATCGAAGCACGGTACA
742	GATTCGGACAGCACGGCATA
743	GCTCCGGCAGTCACGATTAA
744	GACTGTCGAGCACCCATTGA
745	GATCGTCGAGCACGCCTAAT
746	GAGGTCAGACGACGCCTATA
747	GCGCGTATAGCTCTCCATAG
748	TAGCGAGTAGCACTTCGATA
749	CTAAGTGTAGCACCACATCA
750	GTAGATCGAGCAGCCAGTCT
751	GACATAGACCATACCACGTT
752	CGTCTTCGAGCAAGTGCAGT
753	CTCTCCGGCAGCGATATGTA
754	CCCTCAGCACGAGATATAAG
755	CCCTTGCGAAGCATTGCGAA
756	CTCCAGGCAATGAGAGCACA
757	CCCAGATCAAGCGATGCAGA
758	CTGAATCCAATGTACGTGAC
759	CGGCATTCAAGGTAGCGACA
760	GCCCGATTAAGGTGTCAA
761	GCCCGATCAATGGCTGCATA
762	CGCCATCCAAGGGCTGTATA
763	CGGATGCCAAGGGCTTCATA
764	GGTTGCGCCAGGTCATCTTA
7 6 5	GGTCCGGCATGGATCACTAA
766	GGCTGGCACATGATCGTATA
767	TGGTTGCACTTGGATCGAAA
768	TGATTGCACTTGGATCGAAA
769	TGTTGATCCATGTCCATACG
770	TTAAGGCACTTGATCTCAGC
771	GTAATGCCTGGACCGCAAT
772	GTTAAGCCTTCCACGGCAAT

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Seq. Id	3' to 5' sequence
773	GTTGCGCCATTGAGCCAGAT
774	GTTGCCCACCTGAGACGTTA
775	AATGCGCCACAAAGCGAGTG
776	CACCGGCCAAGAAGTACAGT
777	CATCCGCCAAGCAGAGTGAA
778	CGTTGCCAATGCACGAGCTA
779	GATGGCTGAATGACGTTTAC
780	GATTGCCTAATGAGTCTGAC
781	AATCAGCCAAAGATGTGGGC
782	AATCATGCACAAAGTTCGCC
783	ATTTAGGCAAGAAGCGCACC
784	AATTGGCTAAAGAGCGCACC
785	ACATTGGCAAAGCGAACTCC
786	AATGGGAGAAAGCCGACTCT
787	TGTGCTGGAGCTTCAGTCAC
788	GTTGTGCAGGATTATCGACA
789	GCTTGCAGACGAGTCATCAC
790	GGATGGATACTAGCGACTCC
791	GCTATGGCACAGGCATCTAC
792	GGACTGGCACATCCCGTATA
793	GGATCGGACCATTCTCACTA
794	GGATGGCGACATGCTCACTA
795	GAGCTGGCAATCGTCGTACT
796	GGATGGCTACATGATCTGAT
797	GGCAGCAATTCGGGCTAATA
798	GCCTAGCAATGTTCCCAGAG
799	GAGCGGCAATGATGATCCAT
800	TGGTGCATAGCTGCGATCCA
801	GGCTGCACAGGTGTATCCAA
802	GAGATGCCAATCGGCCATAA
803	TATATGGCACATCGTTGCGA
804	TGATGCCCACGTCGTCGTAT
805	ATTGATCCACACAGTACG
806	AGCTGATCCAAGCAACGTAC
807	GTTGATGCAGATCGCGTATC
808	TCGTGGGCAGATCGCTTCAT
809	TGTGGCCGAGATGCCTTCTA
810	TTTGCGGACTTCGCTATCAA
811	TCCCATGCACCTGAGTGGAT
812	TTTCATGGAGCTGTCGCGTA
813	TTTACCTGTGGTGATAGCGA
814	TTGTCATGCTGCCCAGTCGA
	CTTTCATGCAGGCAGAGCCA
	CCTTTAAGCTGGCACACGAT
	CCTATCAAGGATGCACACGA
	CCGTTCAGAATATGACACAC
819	TAGGTCAGATCATGCGCGAC
820	ATGTGCATACAAGCTACGAC

Seq. Id	3' to 5' sequence
821	CTGAGAATATGAGAGACGCC
822	ACTCACGCAAATGAACGGCG
823	CTTAGCGAATATGCGATACG
824	ACTCTGATAAATCCGACACG
825	ACTGTGCGAAATCCCAGACA
826	ACTGATGTAAATCCACACCG
827	ACGTGAACAATTCCACACTG
828	ACTGCACGAAATCGACATCG
829	ACTTCTGTAAATCGCAGCAC
830	CTGTCTTGAATAGCGATCAC
831	ATGCGGTTAAGCGGTAATAC
832	TACGCTGAGTCATCCGAATA
833	CTTGTGAGACACTCCGACAT
834	CTGGTGACATACTATCAGAC
835	CGTGCGTTAAGCTGTCGATA
836	CGGTATCGAAGCTGCGTATA
837	CGCGTGTGAAGCTGCCTATA
838	CCTAGTAGAAGCTCCACAGA
839	TGTGTCGGAGTCGCCCATAT
840	TCTGTCGAGGTAGGCCATAT
841	GCTGTCGAGAGCGATCATCA
842	GCAGTCGGACGAGATTCTAC
843	GCGATGGTACTAGATCAGCA
844	GTGTAGGGACTCGTATCACT
845	GTACGAGCAGTTGAGCATAA
846	GTCAGTCGAGATTCAGCAGT
847	GTCGAGTCAGATGCACGTCA
848	GTGTATCTAGCTGCACGCAC
849	GTTGTCTTACGTGCAGTCAG
850	TATGTACTCGTATCGACGCA
851	TCGTGTCGAGTATCCGCAAA
852	GTACGTTGACAGTCTGCACA
853	TTCGTAGAGGTCTGCCAATT
854	ATTCTGAGAGACAAGCCTCC
855	ATTCTGACACAATCATCGCG
856	ATTCAGAACTAATGCACCGC
857	AGGTATGAACCATCGCACAC
858	ATTTGATGAACTCCGCAGAC
859	GTTTGCTGACCTCGCAGTCT
860	ATTGCCGGAACGCATTATAC
861	TGTGTGGGATCGCCCTATCT
862	TTGAGTGAGCTGCGCTTATA
863	TGCGTGCAGGTGCCACTAAA
864	GTGCTGCATGAGCCAGTTCA
865	GGCTCTACATGGCGATAGCA
866	GCTCTCTAATTGCGGACACA
367	GGATATAAGTTGCGGCACTA
368	GGATGTAATGGTAGCTCCTA

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Seq. Id	3' to 5' sequence
869	GGATGACGAGGTCTCACCAT
870	GGATGCGACGATCTCGACAT
871	CGTGATCGAAGGCTGCACAA
872	CTAGATGTAAGTAGCTGGAC
873	CGAATGAAGGATCGAGACCT
874	CGGCCTGGAAGTCACTCATA
875	GGCCTTGGACTACCGCTTAA
876	TGCTTCGAGGGTCCCACTTA
877	TGCCTGGTACTGTCCGACTA
878	TGCTTGTGAGAGTCGCTACT
879	ATGCTTGCAGAACCGTCAGC
880	TGACTGTAGGGAGCCTCAAC
881	TGCTTGGCAGGATGTCTTAA
882	GGCTCCGGCATGAGTATATC
883	TGCTTTGCAGTGAGGCTCTC
884	CAATTTGGAACTAGCCTTCG
885	TTTGCTGCATCCGGCCTGTA
886	TTGGGCCACTGCGCTCTTTA
887	TGTGAGCCCTTGGCACGTTA
888	GGTGGCCCGATCACATTCAA
889	GGCAGGCACCTCAGTTTAT
890	GGGTGGCCCATGCTATCTAA
891	GTCTGGCCCTACCTATGGTT
892	GCGGCACACCTCTGATTTA
893	GCGGCCACCATTCATTAT
894	GGAGCCCACCATGAGCTATA
895	GAATCTCCACCAGGCGGATA
896	GGATACGTCGCTACAGTGAT
897	TCGTATAGCTGTATCGACGG
898	CTAACTAGCTGTAAGCGACC
899	ACTAGATAACAGATGCGCCG
900	CAACTATCATCAAGACGGCG
901	CAACAGAGATGAAGCGCGTC
902	CAACATATCATAAGCGCGTC
903	GCAGATAGCATCATATACGC
904	GCAGACTGAATTAGCTCTAC
905	GTTAATTCATCTAGCGCGAC
906	AGGAATCTAACCACGCGCAG
907	AGACCAATAAGCACCCTGGG
908	AGACAAACATTCACGCCGGG
909	AGAATAAATTACTGCCCGGC
910	GAGCACATATTATTACGCCC
911	CAGAAGATAATATGCTCGCC
912	GAATAGCCGATAATCTCAGC
913	GAATAGCTTTACACTGCCCT
914	GAATCACTCTGAATGAGCAC
915	GGATCACACTGCCGGACTAT
916	GGACCCATAGCACTCTGATT

\neg
$\neg \neg$

Seq. Id	3' to 5' sequence
965	TGACTACCGTGTCGCATACG
966	TGGACTACGTGTCTCGATAG
967	TAGTGATACTGACTCATGGC
968	CGTCTGATACAGCCCAGTGT
969	GCCGTATCACGACGCTAGAT
970	AGCTCGATACAACGCTAGAG
971	ATCTACTTAACGCGCTACAG
972	GACATCGTACCACTGCGTAG
973	GACTCGTGACCACTCTGTAG
974	GACTCGGACCATATCTACGG
975	CACTACGCAAGACTATGTAC
976	CGAGTCTCACAGCAATCTAG
977	CGATCTAGCACGCAATATAC
978	GACCAGCGACGACAGTAGAT
979	CGTAGACAGCCACGCAGTTA
980	CGTATGCTACCACCGATTAT
981	CGTGCGATACCAGCGTAGAT
982	CTCCGTACAGCAGGCAGTAT
983	CTCGTCGTACAGCGATCAGT
984	CTACAGATACGTCGAGAGAG
985	CTACGCGACACGCATGAGAT
986	TAGACGCTCGCACGGTAGTA
987	GCCGCTAGACGACGGTATAT
988	GTATCACTAGGACGAGGTAT
989	GTACTCACAGTGCGAGAGCT
990	CGACTACACAGCTCAGGATA
991	CACCGACAACTCGTAGAGAG
992	CGACCCACACTAGGAGAGAT
993	ACGCGCACAACAGGAGACTT
994	AGTACCACAACTCAGACGTG
995	AGTACAGCAACGCAGAGCCT
996	GTCAGCGACCGTCAGCTATT
997	GTCAGGCACTAGGAGCTATC
998	TGTCGGTCACTCCTGGACTA
999	TCGGTTCACGTCCGCATGTA
1000	TCGTTTACCTGTCGCGCTGA
1001	TGTGTCTCACTTCCGCGAGT
1002	TCTGAGCACTCTCTCGTAGG
1003	GTTGATGACTCGCCACACGT
1004	CTGAGATCACAGCAGACTAG
1005	TTAGACTCCTCGCCGGTAGA
1006	TATAGCTCCTAGCAGGCGTA
1007	TATGCTCCACGTCTAGTGAG
1008	CTCTATCACCAGCGATGAGA
1009	CGCTCCAGACAGCATATAGA
1010	ACATACCGAAAGCTCTAGCG
1011	ACATCGCTAAAGCACATCGG
1012	ATATCGCGCAATCAACGCTA
1012	MINICACACATONACACTA

Soa Id	O' to E' angueros
Seq. Id	3' to 5' sequence
1013	CGATGCGCCACTCAAGGTAT
1014	TATGCCGACGGTCAGGCTAA
1015	TATCGCCACGTCCGGTGATT
1016	TCTCGCTCACTGCGTATGAT
1017	TATCCGTCACTCCGTAGAGG
1018	TATCGACTATCCCTGAGACG
1019	GTATAGACCTCTCAGACGCG
1020	CTATCGTAATATCAGTCCGC
1021	CGATGACAATTAGGTACACG
1022	GAGCATAATGACGTAGACCG
1023	CGACAATACTTGACAGCACG
1024	CGATGATAATAGAGTAGCCG
1025	CTATGATTAAGTCGTAGCCC
1026	AGGTGAATAACGCATACGCC
1027	GAGTGAGTAATGCTACGTCA
1028	GATCGACGAATGTTAGAGAC
1029	GACTCACGAATGCGGAGACT
1030	GACCGTCAATCGCGTCAGAT
1031	TACCCGCATCGACGGAGTTT
1032	GTCAGCGCACTCCTGGTTTA
1033	TCAGGCCCACGTAGCGTTAT
1034	TTCGCGCTATCCATGCGTGA
1035	TGCTGATACTCGGCTGCATC
1036	TGAGTAGCATCGGTGACTTC
1037	TTGTATCACTGTGCTGCCCA
1038	TTTAGTCAGTATGCTCGCGG
1039	TTACGTTTATATGGCCGAGG
1040	TGAGATCACGTTCGCCGAGT
1041	GTATCATTAGCTCCGCAGAG
1042	TATCATGTAGACTCGGAGGC
1043	GTATGCTTAGATATGCAGCG
1044	TTGTAGTTAGCTCTGCACGG
1045	ATATCGTTAAGCCATACGCC
1046	ATTCTGATAACGCTCTCGAC
1047	ATTCGTCCAACGCGGTCGAT
1048	ATATGCACAACGCGCAATCG
1049	TTAGCTCTATCGCAGTCCGA
1050	ATTAGCTGAACGCCTCGCAA
1051	ATTATCTCAACGGAGGAGCA
1052	ATGTTGCTAACGGACGGACA
1053	ATGTGTTCAACGGAGACAGA
1054	CTCTTCTAAGTGAGTCGAG
1055	CTGCTTGAAGTCGTCTCACG
1056	CTGCGTTGAAGTGGCTTACT
1057	GTGCGTTCACATGGCCGTAT
1058	GTAGCCGCACCTGACTGTAT
1059	GTAGCGCCACCTGACGTTAT
1060	GGCGCGTCACATGATACATT
1000	adodod Choh Tah Thoh T

Seq. Id	3' to 5' sequence
1061	GGTTGCTACGATGACTCAGT
1062	GAAGGCCGTACACTCTATA
1063	GACAGGCACACGACTCTAT
1064	TGCGCGCACTCGTTCTATA
1065	GCGGTTGCACTCGTAGCATA
1066	GAGGCGTGACCAGTCCATAT
1067	GGACGCTCACCAGTCCATAT
1068	AGTGTCCAACCAGACCAGAG
1069	AGTGCCATACAAGCGCATAG
1070	GTAGCCTTACATTGGCAGAG
1070	GTCGCCGCACATTCGGTTAT
1071	GTTGAGTCAGATTAGCAGTC
1072	TCGTAGGGACTGCGCTCATA
1073	CTCAGATGACAGCGACGCAT
1075	CTCTGAGGACAGCCGAATCT
1076	CTAGGATGACAGCCAGACAC
1076	CGTGAATTACATCAGACAGC
1077	CTGATTACATCAGACAGC
	CTAATATGATGACAGTCCGC
1079 1080	TACTTATGATGACAGTCCGC
1081	GAACTATGCTGACGACACACACACACACACACACACACAC
1082	CGATTCTGACCACACACAC
1083	CTAATCTGACCACGAGACGA
1084	CTGTATTGACATCAGACGAG
1085	CTTCTCAGACATCGGACGAG
1086	GCACTGTGAATTAGCGAGCA
1087	GCCTACGGAATTGGCAGACT
1088	GACCTGGAATTAGCACACGC
1089	GCCTGCGAATTAGCGGACAT
1090	GCGATGCTAATGATGTGTAC
1091 1092	GCCCGTCTAATGAGTGGACA
	GCCTAGCTCATCAGACGAA
1093 1094	GCATGGACATCCTACGAGAA
	CGCCTGCCAAGCTGTGATAT
1095	GCCTGCGCCATCAGTAGATA
1096	GCACGCCAATTACTCGATA
1097	GCAGCGAGACCATGTGATAC
1098	GCAGCAGCACACTGATCGTT
1099	GACCCAGCACATTAGCGAGA
1100	GCTCCTGCAATGTGCGGATA
1101	GCGCCTGAATTGTAGCACGT
1102	GCCACAGCATTGGAGAGAAT
1103	GCCAGGCTAATGGATAGTAA
1104	GCCCTGCGAATGAAAGACAT
1105	GCAGCGGGAATTAGATATAC
1106	GCAGGTGCAATGATTCTACC
1107	GACCGGGCAATCACTTCAGA
1108	GCCGGCAATGCGTTCATAT

1109 CCCAGGGCAAGCGATCATAA 1110 GCCACAGGCAGGCATATTA 1111 GCCTAATCCTGGGACACTGA 1112 TCGTCTCGATCTAGGCCATG 1113 GTGTCTCGACTCAGCCTATA 1114 GACGTAGTAATCATGTCTCC 1115 GACTTATACGTCATGCGACC 1116 ACGATGTAACACAGCGACCG 1117 AGTCGTGACACAGCGACCG 1117 AGTCGTGACACAGCGACCG 1118 GTCGTGACAGTGACA 1118 GTCGTGACAGTGACA 1119 GTGGAGTGACAGTGACA 1110 GTGGAGTGACAGTGACA 1111 GTCGTGCAGACTCTCAA 1120 TAGAGGTGACGTATCTCTAA 1120 TAGAGGTGACGTAGTCCACT 1121 GTCGTGCGAGATAGCCACT 1122 GTGTAGAGATAGCATCGC 1123 TAGTCGTGAGATAGCATCGC 1124 CAGTGTACAGATACGAAG 1125 CGAGTGTCACATACCACATA 1126 CGTATAGCAGACAGCGCAAT 1127 GACATCGACGACAGCACATA 1128 CGAAGCTCACGTAAGTCAAG 1129 TAGTGCTCACGTAGCCCAGT 1130 TGCCCACGGTGAGCTAGTT 1131 TAGCTGCCAGGAGCAGCTTCA 1132 TCGGCTACGTAGCACACA 1133 TAGGGTACTGATGAGACACCC 1134 CTACGGGAAGGTTAGCACCA 1135 TGGTGATACCACTGCCCACA 1136 GATTAGATACCACTGCCCCA 1137 GGAGTGATACCACTGCCCCACA 1138 AGCTGACGAAATCTTCACAC 1139 GAGGAGATAACCACTGCCACA 1131 GGAGTGATACCACTGCCACA 1131 CACGGGAAGATACCACTACCCCC 1132 CACGGAAGATACCTCGATCCAC 1133 TAGGGTAACCTTGATCACCCCCC 1134 CTACGGGAAGATATCTCACAC 1135 TGGTGATACCTCGATCCAC 1136 GATTAGATACCACTGCCACA 1137 GGAGTGATACCTCGATCCAC 1138 AGCTGACGAAATCTTCACC 1139 GAGGAGATAATACATCCTCG 1141 ACACGCAACAAGTCGACCGT 1142 CACGGAATAATACATCCTCG 1143 CAAGAGATAATACATCCTCG 1144 CAAGCAACAAGTCGACCCTC 1145 ATAAGCGCAACAAGTCAGCCTC 1146 ATCTGAGCAACAAGTCAGCCTC 1147 CACAGGCTAAGACAGCTACC 1148 CAAGCCTAAGACAGCTACC 1149 CATAGTTAAGCACAACAAGTCAGC 1149 CATAGTCTAAGACAAGCAACAGCAGCT 1149 CATAGTCTAAGCCACATCAG 1150 GACAGTACATGCCAATCAGC 1141 CAAGCGAAAACAAGCCAACAAGTACAGC 1142 CAAGGCTAAGACAAGCAACAACAGCAGCT 1143 CAAGAGATAATACAGCCACCATCAG 1144 CAAGTCTAAGCCACAACAAGCAGCGT 1145 ATAAGCGCAACAACTAGGACAGCTACAG 1150 GACAGTACATGCCAATCAGC 1141 CAAGCGAAACAACTAGGACAGCTACAACAACAGCCAACAACAAGCAACAACAACAACAACAAC	Seq. Id	3' to 5' sequence
1110 GCCACAGGCAGGCATATTA 1111 GCCTAATCCTGGGACACTGA 1112 TCGTCTCGATCTAGGCCATG 1113 GTGTCTCGACTCAGCCTATA 1114 GACGTAGTAATCATGTCTCC 1115 GACTTATACGTCATGCGACC 1116 ACGATGTAACACAGCGACCG 1117 AGTCGTGAACACAGCGACCG 1118 GTCGTGACAGTGATGACA 1118 GTCGTGACAGTGATGACA 1119 GTGGAGTGACAGTGATCACTCTAA 1120 TAGAGGTGACGTATCTCTAA 1120 TAGAGGTGACAGTAGTCCACT 1121 GTCGTGCGAGATAGCTCTTA 1122 GTGTAGAGATATAGCATCGC 1123 TAGTCGTGAGAATAGCATCCC 1124 CAGTGTGTACGAATACCACATA 1125 CGAGTGTACCACATAACCACATA 1126 CGTATAGCAGACAGCGCATA 1127 GACATCGACGACAGGCCATA 1128 CGAAGCTCACGACAGGCCATA 1129 TAGTCGTCACGTAGCACAGCCCAGT 1130 TGCCCACGGTGAGCTAGTTT 1131 TAGCTGCCAGGAGAGCTAGTTT 1131 TAGCTGCCAGGAGGCGTATTT 1132 TCGGCCTACGTTGCATTAA 1132 TCGGCCTACGTGAGCACACCCACACCCCCCCCCCCCCCC		
1111 GCCTAATCCTGGGACACTGA 1112 TCGTCTCGATCTAGGCCATG 1113 GTGTCTCGACTCAGCCTATA 1114 GACGTAGTAATCATGTCTCC 1115 GACTTATACGTCATGCGACC 1116 ACGATGTAACACAGCGACCG 1117 AGTCGTGTAACCATGTGACA 1118 GTCGTGACAGTGATACTCTC 1119 GTGGACGTATCTCTAA 1110 TAGAGGTGACGTATCTCTAA 1110 TAGAGGTGACGTATCTCTAA 1120 TAGAGGTGACGTATCTCTAA 1121 GTCGTGCGAGATAGCCCTT 1121 GTCGTGCGAGATAGCCCTT 1122 GTGTAGAGATAGCATCGC 1123 TAGTCGTGAGATAGCATCGC 1124 CAGTGTGACATACCACATA 1125 CGAGTGTCACATACCACATA 1126 CGTATAGCAGACAGCGCAAT 1127 GACATCGACGACAGGCCATA 1128 CGAAGCTCACGTAAGCCACATA 1129 TAGTGCTCACGTAAGCCACAT 1129 TAGTGCTCACGTAGCCCAGT 1130 TGCCCACGGTGAGCTAGTT 1131 TAGCTGCCAGGAGGCGTTCTA 1132 TCGGCCTACGCTGTGCATTA 1133 TAGGGTACTGATGAGCACCC 1134 CTACGGGAAGGTTAGCACCA 1135 TGGTGATACCTGTGCGCCTA 1136 GATTAGATACCACTGCCACA 1137 GGAGTGATACCTCGCACA 1138 AGCTGACGAAATCTTCACAC 1139 GAGGAGAATACTCTCACC 1140 CACGGAATAATCCTCG 1141 ACAGCAACAAGTCACC 1141 ACAGCAACAAGTCACC 1142 ACGGAAGAATATCCTCG 1143 CAAGAGATAATACCACCTCC 1144 CAAGTCTAAGACAGCCTC 1145 ACAGCAACAAGTCGAGCCGT 1146 ACTTGAGCCAAGCCGCT 1147 CACAGGAGAAATCTTCACAC 1148 CAAGACAACAAGTCGACCCTC 1149 CAAGACAACAAGTCGAGCCGT 1140 CACGGAATAATACATCCTCG 1141 ACAGCAACAAGTCGAGCCGT 1142 ACGGAGAGAAATCATCCCCC 1143 CAAGAGATAATACATCCTCG 1144 CAAGTCCTAAGACAGCCGT 1145 ATAAGCGCAAGACAGCCGT 1146 ATCTGAGCAACAAGTCGACCCTC 1147 CACAGGCTAAGACAGCCGTC 1148 CAAGACAAGTCAACCAGCCTC 1149 CAAGACAACAAGTCGACCACCTC 1140 CACGGAATAATACCACCCTC 1141 CAAGCCAACAAGCCACCCTC 1142 ACGGAGAGAAATCAGCCACCCTC 1143 CAAGACAAATAACAACCACCCTC 1144 CAAGTCCTAAGACAAGCCACCCTC 1145 ATAAGCGCAACAACAAGCAGCCTC 1146 ATCTGAGCCAAACAAGCAACCAACCAGCCTC 1147 CACAGGCTAAGACAAGCAACCAACCAGCCTC 1148 CAAGCCTAAGACAACCAACCAACCAGCCTTCAC 1151 GCGCTAATCACCCACAACAACCAGCCTTCAC 1151 GCGCAATCACCCACCACCACCACCATCAG 1152 GGGAGTAATACCTCGACCACCACCACCACCATCAG 1155 GACAGTACACCACCACCACCACCACCATCAG 1155 GACAGTACACCACCACCACCACCACCTTGATT 1155 GGCGCATCACACACCACCACCACCACCTTGATT 1155 GGCGCATCACACACCACCACCACCACCTTGATT 1155 GGCGCATCACACACCACCACCACCACCTTGATT 1155 GGCGCATCACACACCACCACCACCTTGATT 1155 GGCGCATCACACACCACCACCACCTTTGTT 1155	<u> </u>	<u> </u>
1112 TCGTCTCGATCTAGGCCATG 1113 GTGTCTCGACTCAGCCTATA 1114 GACGTAGTAATCATGTCTCC 1115 GACTTATACGTCATGCGACC 1116 ACGATGTAACACAGCGACCG 1117 AGTCGTGTAACCATGTGACA 1118 GTCGTGACAGTGATACTCTCA 1119 GTGGACGTGACA 1119 GTGGAGTGACGTATCTCTAA 1120 TAGAGGTGACGTATCTCTAA 1121 GTCGTGCGAGATAGCTCTTA 1122 GTGTAGAGATAGCTCTTA 1122 GTGTAGAGATAGCATCGC 1123 TAGTCGTGAGATAGCATCGC 1124 CAGTGTGACAATACGAAG 1125 CGAGTGTACCACATA 1126 CGTATAGCAGACAGCGCAAT 1127 GACATCGACGACAGCGCAAT 1128 CGAAGCTCACGTAAGCACAGA 1129 TAGTGCTCACGTAAGCCACAT 1129 TAGTGCTCACGTAAGCCACAT 1130 TGCCCACGGTGAGCTAGTT 1131 TAGCTGCCAGGAGAGCGCATA 1132 TCGGCCTACGCTGTGCATTA 1133 TAGGGTACTGATGAGACACC 1134 CTACGGGAAGGTTAGCACCA 1135 TGGTGATACCACGTGCCACA 1136 GATTAGATACCACTGCCACA 1137 GGAGTGATACCTCGCCACA 1138 AGCTGACGAAATCTTCACAC 1139 GAGGAATAATCCTCGATCACC 1140 CACGGAATAATCCTCG 1141 ACAGCAACAAGTCACC 1142 ACGGAAAATCTTCACAC 1143 CAAGAGATAATACATCCTCG 1144 CAAGTCTAAGACAGCCTC 1145 ATAAGCGCAAGACAGCCGT 1146 ACTGAGCAAAATCATCACCC 1147 CACAGGAGAAATCTTCACAC 1148 CAAGAGATAATACATCCTCG 1141 ACAGCAACAAGTCGAGCGTT 1142 ACGGAAGAAATCTTCACAC 1143 CAAGAGATAATACATCCTCG 1144 CAAGTCTAAGACAGCTACG 1145 ATAAGCGCAAGACAGCGCTC 1146 ATCTGAGCAAAATATACATCCTCG 1147 CACAGGCTAAGACAGCCGTC 1148 CAAGACAAGTCGAGCCGT 1149 CAAGACAAGTCGAGCGTT 1149 CACAGGAAAATATACATCCTCG 1141 ACAGCCAAAAATAACAACCCTC 1142 ACGGAAGAAAATAACAACCCTC 1143 CAAGAGATAATACAATCCTCG 1144 CAAGTCTAAGACAAGCCACC 1145 ATAAGCGCAAGAACAAGCAGCCTC 1146 ATCTGAGCCAAACAAGCAGCCTC 1147 CACAGGCTAAGACAAGCAGCCTC 1148 CAAGACAAATAACAACCACCACCCTC 1149 CAAGACAAACAACAACAACAACAACAACAACAACAACAAC		
1113 GTGTCTCGACTCAGCCTATA 1114 GACGTAGTAATCATGTCTCC 1115 GACTTATACGTCATGCGACC 1116 ACGATGTAACACAGCGACCG 1117 AGTCGTGTAACCATGTGACA 1118 GTCGTGACAGTGACA 1119 GTGGAGTGACGTATCTCTAA 1120 TAGAGGTGACGTAGTCACT 1121 GTCGTGCGAGATAGCTCTTA 1122 GTGTAGAGATATACGCTTTA 1122 GTGTAGAGATATAGCATCGC 1123 TAGTCGTGAGATAGCATCC 1124 CAGTGTGAGATAGCATCG 1125 CGAGTGTCACATACCACATA 1126 CGTATAGCAGACAGCGCAAT 1127 GACATCGACGACAGCCATA 1128 CGAAGCTCACCATACCACATA 1129 TAGTGCTCACGTAAGTCAAG 1129 TAGTGCTCACGTAAGTCAAG 1129 TAGTGCTCACGTAGCCCAGT 1130 TGCCCACGGTGAGCTAGTT 1131 TAGCTGCCAGGAGACGCTATA 1132 TCGGCCTACGTTGCATTA 1133 TAGGGTACCTGATGACACAC 1135 TGGTGATACCACTAC 1136 GATTAGATACCACTGCCCAC 1137 GGAGTGATCCTCGATCACC 1138 AGCTGACGAAATCTCACC 1139 GAGGAGATACCTCGATCCAC 1139 GAGGAGATAATCCTCGATCCAC 1139 GAGGAGATAATGGTCACCA 1140 CACGGAATAATACATCCTCG 1141 ACAGCAACAAGTCGAGCCGT 1142 ACGGAGAGAAATCTTCACAC 1143 CAAGAGATAATACATCCTCG 1144 CAAGTCCTAAGACACCC 1145 ATAAGCCCAAGACAGCCCT 1146 ATCTGAGCAAAATCAGCCCTC 1147 CACAGGAAAATCAGCCCTC 1148 CAAGAGATAATACATCCTCG 1149 CAAGACAAAGTCGAGCGT 1149 CAAGACAAACAAGTCGAACCAC 1149 CAAGACAAACTAGACAGC 1149 CAAGTCTAAGACAGCAGC 1149 CAAGTCTAAGACAGCAGC 1149 CAAGTCTAAGACAACAAGCAGC 1149 CAAGTCTAAGACAACAACAGCAGC 1149 CAAGTCTAAGACAACAACAGCAGC 1149 CAAGTCTAAGACAACAACAGCAGC 1149 CAAGTCTAAGACAACAACAGACC 1149 CAAGTCTAAGACAACAACAACAGACAGC 1141 CAAGCCAAAACAACAACAACAACAACAACAACAACAACAA		
1114 GACGTAGTAATCATGTCTCC 1115 GACTTATACGTCATGCGACC 1116 ACGATGTAACACAGCGACCG 1117 AGTCGTGTAACCATGTGACA 1118 GTCGTGACAGTGATGTACTC 1119 GTGGAGTGACGTATCTCTAA 1120 TAGAGGTGACGTAGTCCACT 1121 GTCGTGCAGAGTAGTCCACT 1122 GTGTAGAGATATAGCATCGC 1123 TAGTCGTGAGATAGCGATTC 1124 CAGTGTGACAATAGCATCG 1125 CGAGTGTACGAATACGACG 1126 CGTATAGCAGACAGCGCAAT 1127 GACATCGACGACAGAGCCATA 1128 CGAAGCTCACGACAGAGCCATA 1129 TAGTCGTCACGTAGCCAGA 1129 TAGTCGTCACGTAGCCAGT 1130 TGCCCACGGTGAGCCAGT 1131 TAGCTGCCAGGAGCGCATT 1132 TCGGCCTACGCTGTGCATTA 1133 TAGGGTACTGATGAGCACAC 1134 CTACGGGAAGGTTACAC 1135 TGGTGATACCTGTGCACTA 1136 GATTAGATACCACTGCCACA 1137 GGAGTGATACCTGTGCACCA 1138 AGCTGACGAAATCTTCACAC 1139 GAGGAGATAATCCACCAC 1139 GAGGAGATAATCCACCCAC 1131 GAGGTACCTCGACCAC 1131 CACGGAAATCTTCACAC 1131 CACGGAAATCTTCACAC 1131 CACGGAAATCTTCACAC 1131 CACGGAAATCATCACCCACAC 1131 CACGGAAAATCATCCCCCACACC 1131 CACGGAATAATACCACTCCCCACACCCCCCCCCCCCCCC		
1115 GACTTATACGTCATGCGACC 1116 ACGATGTAACACAGCGACCG 1117 AGTCGTGTAACCATGTGACA 1118 GTCGTGACAGTGATGTACTC 1119 GTGGAGTGACGTATCTCTAA 1120 TAGAGGTGACGTAGTCCACT 1121 GTCGTGCGAGATAGCTCTTA 1122 GTGTAGAGATAGCATCGC 1123 TAGTCGTGAGATAGCATCG 1124 CAGTGTGACAATACCACATA 1125 CGAGTGTACGAATACCACATA 1126 CGTATAGCAGACAGCCAAT 1127 GACATCGACGAAGCAAT 1128 CGAAGCTCACATAACCACATA 1129 TAGTCGTGAGACAGCCAAT 1129 TAGTGCTCACGTAGCCAGT 1120 TAGTGCCACGTAGCCAGT 1121 GACATCGACGACAGCCAAT 1122 GACATCGACGACAGCCCATA 1123 CGAAGCTCACGTAGCCAGT 1130 TGCCCACGGTGAGCTAGTTT 1131 TAGCTGCCAGGAGCGTTCTA 1132 TCGGCCTACGCTGTGCATTA 1133 TAGGGTACTGATGAGCACCC 1134 CTACGGGAAGGTTAGCACCA 1135 TGGTGATACCTGTGCGCCTA 1136 GATTAGATACCTCTGCCCACA 1137 GGAGTGATACCTGTGCGCCTA 1138 AGCTGACGAAATCTTCACAC 1139 GAGGAGATAATCACCCCCC 1140 CACGGAATAATCACCCCG 1141 ACAGCAACAAGTCGAGCCGT 1141 ACAGCAACAAGTCGAGCCGT 1142 ACGGAAGAAATCTTCACCC 1144 CAAGTCCTAAGACAGCCCTC 1144 CAAGAGATAATACACCCCCC 1144 CAAGACAACAAGCCGCCTC 1145 ATAAGCGCAAGACAGCAGCCTC 1146 ATCTGAGCCAAGACAGCAGCCTC 1147 CACAGGCTAAGACAGCAGCCTC 1148 CAAGAGATAATACAGCCCTC 1149 CATAGCCTAAGACAGCAGCCTC 1140 CACAGGCAAGACAGCAGCCTC 1141 CAAGACAACAAGACAGCAGCCTC 1142 ACGGAAGAAAATCAGCCCTC 1143 CAAGAGATAATACAGCCACCTC 1144 CAAGTCCTAAGACAAGCAGCCTC 1145 ATAAGCGCAAGACAGGAGCT 1147 CACAGGCTAAGACAGGAGCT 1148 CATAGCGTAAGCCAACAACAGAGACG 1149 CATAGTCTAAGCCACAATCAGC 1151 GCGGTAATCGGTGCCATCAA 1152 GGGGAGTATAGCCACAATCAGC 1151 GCGGTAATCGGTGCCATCAA 1152 GGGGAGTATAGCTGACCATCAA 1153 GTAGGCAGACCACCATCAA 1154 GAGCCAGACCACCATCAA 1155 GGCGCATCACTAGCCAGATT 1156 GAGCCAGACCACCACCATCAA 1157 GAGCCAGACCACCACCATCAA 1158 GAGCCAGACCACCACCATCAA 1159 GAGCCAGACCACCACCATCAA 1151 GCGGTAATCGGTGCCTT 1151 GCGGTAATCGGTGCCATCAATCAGC 1151 GCGGTAATCGGTGCATCAATCAGC 1151 GCGGTAATCACCACACTCAATCAGC 1151 GCGGTAATCACCACCACTCAATCAGC 1151 GCGGTAATCACCACACCACCATCAA 1155 GACCAGACCACCACCACCATCAG 1155 GACCACACCACCACCACCACCATCAG 1155 GACCACACCACCACCACCACCATCAG 1155 GACCACACCACCACCACCACCATCAG 1155 GACCACACCACCACCACCACCATCAG		
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TAGCTGCCAGGAGCGTTCTA 1132 TCGGCCTACGCTGTGCATTA 1133 TAGGGTACTGATGAGCACTC 1134 CTACGGGAAGGTTAGCACCA 1135 TGGTGATACCTGTGCGCCTA 1136 GATTAGATACCACTGCCACA 1137 GGAGTGATACCTCGATCCAC 1138 AGCTGACGAAATCTTCACAC 1139 GAGGAGATAATGGTCACTAC 1140 CACGGAATAATACATCCTCG 1141 ACAGCAACAAGTCGAGCCGT 1142 ACGGAGAGAAATCAGCCCTC 1143 CAAGAGATAATACGGCTGCC 1144 CAAGTCCTAAGACAGCTACG 1145 ATAAGCGCAAGACAGCTACG 1146 ATCTGAGCACAACTAGGACG 1147 CACAGGCTAAGACAGCAGC 1148 CATAGCGCAAGACAGCAGC 1149 CATAGTCTAAGACAGCAGC 1150 GACAGTACATCAGC 1151 GCGGTAATCGGTGCATCAAA 1152 GGGAGTATAGCTGACCATCA 1153 GTAGGCAGACCACATCA 1154 GAGCCAGACCACCTTGATT 1155 GGCGCATCACTAGCCAGATT		
TCGGCCTACGCTGTGCATTA 1133 TAGGGTACTGATGAGCACTC 1134 CTACGGGAAGGTTAGCACCA 1135 TGGTGATACCTGTGCGCCTA 1136 GATTAGATACCACTGCCACA 1137 GGAGTGATACCTCGATCCAC 1138 AGCTGACGAAATCTTCACAC 1139 GAGGAGATAATGGTCACTAC 1140 CACGGAATAATACATCCTCG 1141 ACAGCAACAAGTCGAGCCGT 1142 ACGGAGAGAAATCAGCCCTC 1143 CAAGAGATAATACGGCTGCC 1144 CAAGTCCTAAGACAGCTACG 1145 ATAAGCGCAAGACAGCGTC 1146 ATCTGAGCACAACTAGGACG 1147 CACAGGCTAAGACAGCAGC 1148 CATAGCGTAAGCCAACAGC 1149 CATAGTCTAAGCCACATCAG 1150 GACAGTACATCAGC 1151 GCGGTAATCGGTGCATCAAA 1152 GGGAGTATAGCTGACCATCA 1153 GTAGGCAGACCACCTTCATT 1154 GAGCCAGACCACCACTT		
TAGGGTACTGATGAGCACTC 1134 CTACGGGAAGGTTAGCACCA 1135 TGGTGATACCTGTGCGCCTA 1136 GATTAGATACCACTGCCACA 1137 GGAGTGATACCTCGATCCAC 1138 AGCTGACGAAATCTTCACAC 1139 GAGGAGATAATGGTCACTAC 1140 CACGGAATAATACATCCTCG 1141 ACAGCAACAAGTCGAGCCGT 1142 ACGGAGAGAAATCAGCCCTC 1143 CAAGAGATAATACGGCTGCC 1144 CAAGTCCTAAGACAGCTACG 1145 ATAAGCGCAAGACAGCGTC 1146 ATCTGAGCACAACTAGGACG 1147 CACAGGCTAAGACAGCAGC 1148 CATAGCGTAAGACAGCAGC 1149 CATAGTCTAAGCCACATCAG 1150 GACAGTACATCAGC 1151 GCGGTAATCGGTGCATCAAA 1152 GGGAGTATAGCTGACCATCA 1153 GTAGGCAGACCACCTTGATT 1154 GAGCCAGACCACCACTTATT 1155 GGCGCATCACTAGCCAGATT		
1134 CTACGGGAAGGTTAGCACCA 1135 TGGTGATACCTGTGCGCCTA 1136 GATTAGATACCACTGCCACA 1137 GGAGTGATACCTCGATCCAC 1138 AGCTGACGAAATCTTCACAC 1139 GAGGAGATAATGGTCACTAC 1140 CACGGAATAATACATCCTCG 1141 ACAGCAACAAGTCGAGCCGT 1142 ACGGAGAGAAATCAGCCCTC 1143 CAAGAGATAATACGGCTGCC 1144 CAAGTCCTAAGACAGCTACG 1145 ATAAGCGCAAGACAGCGTC 1146 ATCTGAGCACAACTAGGACG 1147 CACAGGCTAAGACAGCAGC 1148 CATAGCGTAAGCCAACCAGC 1149 CATAGTCTAAGCCACATCAG 1150 GACAGTACATCAGC 1151 GCGGTAATCGGTGCATCAAA 1152 GGGAGTATAGCTGACCATCA 1153 GTAGGCAGACCACCTTGATT 1154 GAGCCAGACCACCTTGATT 1155 GGCGCATCACTACCACACCACATCACC 1151 GCGCATCACACCACCTTGATT 1155 GGCGCATCACTAGCCAGATT		
1135 TGGTGATACCTGTGCGCCTA 1136 GATTAGATACCACTGCCACA 1137 GGAGTGATACCTCGATCCAC 1138 AGCTGACGAAATCTTCACAC 1139 GAGGAGATAATGGTCACTAC 1140 CACGGAATAATACATCCTCG 1141 ACAGCAACAAGTCGAGCCGT 1142 ACGGAGAGAAATCAGCCCTC 1143 CAAGAGATAATACGCCTC 1144 CAAGTCCTAAGACAGCTACG 1145 ATAAGCGCAAGACAGCTACG 1146 ATCTGAGCACAACTAGGACG 1147 CACAGGCTAAGACAGCAGC 1148 CATAGCGTAAGACAGCAGC 1149 CATAGTCTAAGACAGCACC 1150 GACAGTACATCAGC 1151 GCGGTAATCGGTGCATCAAA 1152 GGGAGTATAGCTGACCATCA 1153 GTAGGCAGACCACCTT 1154 GAGCCAGACCACCTT 1155 GGCGCATCACTACCAC		
1136 GATTAGATACCACTGCCACA 1137 GGAGTGATACCTCGATCCAC 1138 AGCTGACGAAATCTTCACAC 1139 GAGGAGATAATGGTCACTAC 1140 CACGGAATAATACATCCTCG 1141 ACAGCAACAAGTCGAGCCGT 1142 ACGGAGAGAAATCAGCCCTC 1143 CAAGAGATAATACGGCTGCC 1144 CAAGTCCTAAGACAGCTACG 1145 ATAAGCGCAAGACAGCTACG 1146 ATCTGAGCACAACTAGGACG 1147 CACAGGCTAAGACAGCGCT 1148 CATAGCGTAAGACAGCAGC 1149 CATAGTCTAAGCCAAGCAGC 1150 GACAGTACATCAGC 1151 GCGGTAATCGGTGCATCAAA 1152 GGGAGTATAGCTGACCATCA 1153 GTAGGCAGACCTGATCCCTT 1154 GAGCCAGACCACACTAGCT 1155 GGCGCATCACTAGCCAGATT		
1137 GGAGTGATACCTCGATCCAC 1138 AGCTGACGAAATCTTCACAC 1139 GAGGAGATAATGGTCACTAC 1140 CACGGAATAATACATCCTCG 1141 ACAGCAACAAGTCGAGCCGT 1142 ACGGAGAGAAATCAGCCCTC 1143 CAAGAGATAATACGGCTGCC 1144 CAAGTCCTAAGACAGCTACG 1145 ATAAGCGCAAGACAGCGTC 1146 ATCTGAGCACAACTAGGACG 1147 CACAGGCTAAGACAGCAGC 1148 CATAGCGTAAGCCAAGCAGC 1149 CATAGTCTAAGCCACATCAG 1150 GACAGTACATCAGC 1151 GCGGTAATCGGTGCATCAAA 1152 GGGAGTATAGCTGACCATCA 1153 GTAGGCAGACCTGATCCCTT 1154 GAGCCAGACCACCTTGATT 1155 GGCGCATCACTAC		
1138 AGCTGACGAAATCTTCACAC 1139 GAGGAGATAATGGTCACTAC 1140 CACGGAATAATACATCCTCG 1141 ACAGCAACAAGTCGAGCCGT 1142 ACGGAGAGAAATCAGCCCTC 1143 CAAGAGATAATACGGCTGCC 1144 CAAGTCCTAAGACAGCTACG 1145 ATAAGCGCAAGACAGCGTC 1146 ATCTGAGCACAACTAGGACG 1147 CACAGGCTAAGACAGCAGC 1148 CATAGCGTAAGACAGCAGC 1149 CATAGTCTAAGCCACATCAG 1150 GACAGTACATCAGC 1151 GCGGTAATCGGTGCATCAAA 1152 GGGAGTATAGCTGACCATCA 1153 GTAGGCAGACCTGATCCCTT 1154 GAGCCAGACCACCTTGATT 1155 GGCGCATCACTACC		
1139 GAGGAGATAATGGTCACTAC 1140 CACGGAATAATACATCCTCG 1141 ACAGCAACAAGTCGAGCCGT 1142 ACGGAGAGAAATCAGCCCTC 1143 CAAGAGATAATACGGCTGCC 1144 CAAGTCCTAAGACAGCTACG 1145 ATAAGCGCAAGACAGCGTC 1146 ATCTGAGCACAACTAGGACG 1147 CACAGGCTAAGACAGCAGC 1148 CATAGCGTAAGCCAAGCAGC 1149 CATAGTCTAAGCCACATCAG 1150 GACAGTACATCAGC 1151 GCGGTAATCGGTGCATCAAA 1152 GGGAGTATAGCTGACCATCA 1153 GTAGGCAGACCTGATCCCTT 1154 GAGCCAGACCACCTTGATT 1155 GGCGCATCACTAGCCAGATT		
1140 CACGGAATAATACATCCTCG 1141 ACAGCAACAAGTCGAGCCGT 1142 ACGGAGAGAAATCAGCCCTC 1143 CAAGAGATAATACGGCTGCC 1144 CAAGTCCTAAGACAGCTACG 1145 ATAAGCGCAAGACAGGCGTC 1146 ATCTGAGCACAACTAGGACG 1147 CACAGGCTAAGACAGCAGCT 1148 CATAGCGTAAGCCAAGCAGC 1149 CATAGTCTAAGCCACATCAG 1150 GACAGTACATGCCAATCAGC 1151 GCGGTAATCGGTGCATCAAA 1152 GGGAGTATAGCTGACCATCA 1153 GTAGGCAGACCTGATCCCTT 1154 GAGCCAGACCACGCTTGATT 1155 GGCGCATCACTAGCCAGATT		
1141 ACAGCAACAAGTCGAGCCGT 1142 ACGGAGAGAAATCAGCCCTC 1143 CAAGAGATAATACGGCTGCC 1144 CAAGTCCTAAGACAGCTACG 1145 ATAAGCGCAAGACAGGCGTC 1146 ATCTGAGCACAACTAGGACG 1147 CACAGGCTAAGACAGGAGCT 1148 CATAGCGTAAGCCAAGCAGC 1149 CATAGTCTAAGCCACATCAG 1150 GACAGTACATGCCAATCAGC 1151 GCGGTAATCGGTGCATCAAA 1152 GGGAGTATAGCTGACCATCA 1153 GTAGGCAGACCTGATCCCTT 1154 GAGCCAGACCACGCTTGATT 1155 GGCGCATCACTAGCCAGATT		
1142 ACGGAGAGAAATCAGCCCTC 1143 CAAGAGATAATACGGCTGCC 1144 CAAGTCCTAAGACAGCTACG 1145 ATAAGCGCAAGACAGGCGTC 1146 ATCTGAGCACAACTAGGACG 1147 CACAGGCTAAGACAGGAGCT 1148 CATAGCGTAAGCCAAGCAGC 1149 CATAGTCTAAGCCACATCAG 1150 GACAGTACATGCCAATCAGC 1151 GCGGTAATCGGTGCATCAAA 1152 GGGAGTATAGCTGACCATCA 1153 GTAGGCAGACCTGATCCCTT 1154 GAGCCAGACCACGCTTGATT 1155 GGCGCATCACTAGCCAGATT		
1143 CAAGAGATAATACGGCTGCC 1144 CAAGTCCTAAGACAGCTACG 1145 ATAAGCGCAAGACAGGCGTC 1146 ATCTGAGCACAACTAGGACG 1147 CACAGGCTAAGACAGGAGCT 1148 CATAGCGTAAGCCAAGCAGC 1149 CATAGTCTAAGCCACATCAG 1150 GACAGTACATGCCAATCAGC 1151 GCGGTAATCGGTGCATCAAA 1152 GGGAGTATAGCTGACCATCA 1153 GTAGGCAGACCTGATCCCTT 1154 GAGCCAGACCACGCTTGATT 1155 GGCGCATCACTAGCCAGATT		
1144 CAAGTCCTAAGACAGCTACG 1145 ATAAGCGCAAGACAGGCGTC 1146 ATCTGAGCACAACTAGGACG 1147 CACAGGCTAAGACAGGAGCT 1148 CATAGCGTAAGCCAAGCAGC 1149 CATAGTCTAAGCCACATCAG 1150 GACAGTACATGCCAATCAGC 1151 GCGGTAATCGGTGCATCAAA 1152 GGGAGTATAGCTGACCATCA 1153 GTAGGCAGACCTGATCCCTT 1154 GAGCCAGACCACGCTTGATT 1155 GGCGCATCACTAGCCAGATT	<u> </u>	
1145 ATAAGCGCAAGACAGGCGTC 1146 ATCTGAGCACAACTAGGACG 1147 CACAGGCTAAGACAGGAGCT 1148 CATAGCGTAAGCCAAGCAGC 1149 CATAGTCTAAGCCACATCAG 1150 GACAGTACATGCCAATCAGC 1151 GCGGTAATCGGTGCATCAAA 1152 GGGAGTATAGCTGACCATCA 1153 GTAGGCAGACCTGATCCCTT 1154 GAGCCAGACCACGCTTGATT 1155 GGCGCATCACTAGCCAGATT		
1146 ATCTGAGCACAACTAGGACG 1147 CACAGGCTAAGACAGGAGCT 1148 CATAGCGTAAGCCAAGCAGC 1149 CATAGTCTAAGCCACATCAG 1150 GACAGTACATGCCAATCAGC 1151 GCGGTAATCGGTGCATCAAA 1152 GGGAGTATAGCTGACCATCA 1153 GTAGGCAGACCTGATCCCTT 1154 GAGCCAGACCACGCTTGATT 1155 GGCGCATCACTAGCCAGATT		
1147 CACAGGCTAAGACAGGAGCT 1148 CATAGCGTAAGCCAAGCAGC 1149 CATAGTCTAAGCCACATCAG 1150 GACAGTACATGCCAATCAGC 1151 GCGGTAATCGGTGCATCAAA 1152 GGGAGTATAGCTGACCATCA 1153 GTAGGCAGACCTGATCCCTT 1154 GAGCCAGACCACGCTTGATT 1155 GGCGCATCACTAGCCAGATT		
1148 CATAGCGTAAGCCAAGCAGC 1149 CATAGTCTAAGCCACATCAG 1150 GACAGTACATGCCAATCAGC 1151 GCGGTAATCGGTGCATCAAA 1152 GGGAGTATAGCTGACCATCA 1153 GTAGGCAGACCTGATCCCTT 1154 GAGCCAGACCACGCTTGATT 1155 GGCGCATCACTAGCCAGATT		
1149 CATAGTCTAAGCCACATCAG 1150 GACAGTACATGCCAATCAGC 1151 GCGGTAATCGGTGCATCAAA 1152 GGGAGTATAGCTGACCATCA 1153 GTAGGCAGACCTGATCCCTT 1154 GAGCCAGACCACGCTTGATT 1155 GGCGCATCACTAGCCAGATT		
1150 GACAGTACATGCCAATCAGC 1151 GCGGTAATCGGTGCATCAAA 1152 GGGAGTATAGCTGACCATCA 1153 GTAGGCAGACCTGATCCCTT 1154 GAGCCAGACCACGCTTGATT 1155 GGCGCATCACTAGCCAGATT		
1151 GCGGTAATCGGTGCATCAAA 1152 GGGAGTATAGCTGACCATCA 1153 GTAGGCAGACCTGATCCCTT 1154 GAGCCAGACCACGCTTGATT 1155 GGCGCATCACTAGCCAGATT	1149	
1152 GGGAGTATAGCTGACCATCA 1153 GTAGGCAGACCTGATCCCTT 1154 GAGCCAGACCACGCTTGATT 1155 GGCGCATCACTAGCCAGATT		
1153 GTAGGCAGACCTGATCCCTT 1154 GAGCCAGACCACGCTTGATT 1155 GGCGCATCACTAGCCAGATT	1151	
1154 GAGCCAGACCACGCTTGATT 1155 GGCGCATCACTAGCCAGATT		
1155 GGCGCATCACTAGCCAGATT	1153	
	1154	GAGCCAGACCACGCTTGATT
1156 GGAGCTACATCCGCCAGTTT	1155	
1100 Juanao Indriodadona I I	1156	GGAGCTACATCCGCCAGTTT

Con Id	2' to 5' converse
Seq. Id	3' to 5' sequence
1157	GGAGTCTACCCAGGGCATTT
1158	CGCGCTCTACACGATGGATA
1159	CGTGCCACACCTTGGAGTAT
1160	CGCGGCACACAGTTCAGTAT
1161	GCTCGTCCACAGTGCGTTAT
1162	GCTGACGCAGAGTCCAGTTA
1163	CCGTAGCGACAATCAGCTTA
1164	ACGCACCGAAAGTGAGCGAT
1165	ACGTCCTCAAAGTGCAGACA
1166	ACGCAGTCAAAGTCATATCC
1167	CAGAGTCTAAGATCACCACG
1168	CACTGTCTAAGATACACACG
1169	CAGCGTACAAGCTATACAGC
1170	CCGACGACAATGTACGACAG
1171	GACTAGCGAATCTAATGAGC
1172	CGTCGAGCAATATGAATGAC
1173	CTGTCGCGCACTTCATAGGA
1174	CCGCGACCACGATAGAGAAT
1175	GGCACACGTCTCGGATAA
1176	GGCAGACGACGTTGCATACA
1177	CGTGGGACACAGTCGATCAT
1178	AGTGCGAGAACATCGTGTAA
1179	GGCAGCACAGCTTGTACGAT
1180	GACCATTGAATATGTCGAGC
1181	GTACGCATATTTAGCCAGCA
1182	GGCAATCTGTTCACGACCAA
1183	GCTGACTAATTGCTAGACAG
1184	GGTGTCTAATTGTATGCACG
1185	GTTGACACATTGTTAGCAGC
1186	TTAAGAGATTAGTCTGCCGC
1187	TCACGTAATTTGTTAGCCGC
1188	TGAGTGATAGCTCGGATCTC
1189	ATGATGATAACTACGTGCCC
1190	ATGCGAATAACTATGACGCC
1191	ATGGAGATAACTATGCACCC
1192	TCGTTGCGACCTATGCGTAG
1193	TAGTTCGCACCTACTGCTAG
1194	ATACGTGCAACCACTGCTAA
1195	ATGTCGATAACCTCTGCTAC
1196	ATCTAGTCAACCTGAGCTAC
1197	AGTATAGCAACCTCAACTCG
1198	AAGACACTAAACTCTGCTCG
1199	ACGATAATAACAGCTCCTCG
1200	ATAGATATAACAGCTCCTCG
1201	ACTGTAATAACCAAGCCTCG
1202	ACTGATAGAACCACAGCGCG
1203	ATGGCGACACACATACAGCG
1204	ACGGCGAGAAATACGATGCC

Seq. Id	3' to 5' sequence
1205	GACGCGAGATCAATGTAGTA
1206	CGAGAGTAATCAATCATCCG
1207	CGAGCAATACATACATCTGC
1208	CAACATAGTTACACACGCTG
1209	CAGCTTATAGAGACACACTC
1210	CCATAGAAGTAGACACCTCG
1211	CTCAGAGACATGACACTCGA
1212	ATCAGGTCAACTAATCACCG
1213	AGCGCAGTAAATAGCTTAGC
1214	ACTCCACGAAACATGATTGC
1215	CTCAATATAGACACGATGCC
1216	CGCATTAGAGACAGATCGAG
1217	CGCACATGACATAGAGCACG
1218	CGCACATTAGACAGAGAGGC
1219	CTAGACTAATGCAGAGAGCG
1220	GCGTATAGATGCAGAGATCC
1221	TCACTAGCGTGGAATAGAGC
1222	CAGACTGAACTCAATGTACC
1223	CACGATGAACTAGATGTACC
1224	CGAATGATAAGTATGACGGC
1225	CGAGATGCAAGTATAGTACC
1226	GGATAGCGAGATATAGACCC
1227	GCATAGCACGATGGACGATC
1228	CTCACAGGACATGCAATCGG
1229	TATACATGCTTCGATCACCG
1230	ATATCAATAACTGCGACGCC
1231	AATACGAAAGATGCGGCCCG
1232	ACAGATACAAATGTCGCCCG
1233	ACGAATAGAAATGTGGCCGC
1234	ACATTACTAAAGGTGCGACC
1235	AGATTAGTAAATGCTGCGCC
1236	ACTATGATAACAGCAGCCCG
1237	ATATGAATAACTCCAGCGCC
1238	AGACTGAAATCTACAGCCCG
1239	GTACTGATAATTGGATCGCC
1240	CCAGAACGGTTGCAGACACT
1241	GCAATAGTTGGACCCAGGCT
1242	GGAATAGGTGGACTCACTCA
1243	GCACAAGTTTCGCGCATCGA
1244	GCGGAATCTGTGCAGCATCT
1245	GCGAGAATATGGTGACATCT
1246	GCGGTCAATTAGTGGACTCC
1247	CTCCTACAATGGTGACACTG
1248	CTATTACAATGGTATGCCCG
1249	AATCATACAAAGTGTGCCGC
1250	CATGATCTAAGAGTGTGCCGC
1251	CAAGAAGTAAGATGCGTGCC
1252	CATGTGATAAGATGCGTGCC
1232	DATATAAATATAAAOO

Seq. Id	3' to 5' sequence
1253	AACTTAGCAAACTTAGCGCC
1254	TCTTCGATATGATAGCGTCG
1255	GACGTTAATTGATGAGACGC
1256	GCGTGAAGTTGTTAGCACAT
1257	GCCGATACATGCTGCACGAT
1258	CGCCGATTAAGCTGCGACAT
1259	CGTCATTTAAGTTAGCGCAC
1260	CTCCATCTAAGGTGCGATAC
1261	CGCTTATCAAGGTGCAGACC
1262	GATGACTCAATGTGACTCAG
1263	CGCTAGTGACAATTATGTGC
1264	GCTAGGTGACAGTATGCTAT
1265	GCTGTGCTACGACGTTGACA
1266	GCTAGAGTAGACCGATGCCA
1267	GTATATCGAGATCATAGGCG
1268	GTCTTGGACTATACGAGCGC
1269	TACTTGTAGATAGCGAGCGA
1270	GTACTCTGACATGATTCGCA
1271	TATACTGACCTTATCGGCAC
1272	TCGTCTTGAGATATGTGGAC
1273	TCATGTTACGGTATGCGAGA
1274	TCATCTGCACGTATCGTCAA
1275	GCGACTGGACAGATTGCATA
1276	CGGCCGAAGTATTCACAT
1277	GTGTGGGCACGTATTCCATA
1278	TCCGGGCACGGTGTCATATA
1279	TGGGCGCTACTGGCTCTTAA
1280	TGCGCCGCCAGTCTGTTATA
1281	TGGCCGTTAGAGTCTGCACT
1282	ATGGGCGCAACCCTGTCATA
1283	CAGCCCTGAAGACTGCGATA
1284	CGCCGCTCAAGGCTATGATA
1285	CGCTCCTGAAGGGTAGTTAA
1286	GGCCCGACAGGTGCTATTAT
1287	GGATAGGCAGATGCACTTAT
1288	GGACAGACGTTGACCAGCTA
1289	GTAGCGACATTGAGTTAGCA
1290	GACTACGAATTGAGCATACG
1291	CTACACTAATTGCAGCAGCA
1292	CGTACCCGAATGCAGCAGAA
1293	GACGCCTAATGACGCTGAAA
1294	TAGCTTGTACTGCGACTGAC
1295	GATACTCTAATGCCATCGAC
1296	CGGCGTACAATGCCATAGAA
1297	CGGATACGAAGGCTATGCAA
1298	ACGGATCGAAAGGTATAGCC
1299	ACGGCGCGAAAGCGTCATAA
1300	CGTGAGGGAATACGTCATCA

Seq. Id	3' to 5' sequence
1301	CACAGTGGAAGACGCATCAC
1302	GAGGTGACATGACGTACATC
1303	GAGTAGCGAATGCTCAGCCA
1304	TATAGCACAGTGTCCAGCAA
1305	CGTATGTCAAGGGCCTGATA
1306	CGAGACGCAAGGGATTTACA
1307	GAGACGCAATGTGAATTACG
1308	GATCGCACAGGAGCGTATCA
1309	TGCCAGAGCGTATGAGCAA
1310	TGAGGGCGAGCTATCTATCA
1311	TTGTGGCTAGGTATCGCTAC
1312	TGGTTAGCAGGTATGATCCT
1313	CTCACTGCAAGGATGGGACT
1314	TCCTGTAGATCCCTATGCGG
1315	TCGTTGTCAGCATATTGAGC
1316	ATCATGTGAACCTATTGGCC
1317	TACACTGGGACCTATTGGCC
1318	TACCTGGGACCTATGGGCA
1319	TAGCCCGCAGCATAGCTGAC
1320	GAGCCTCAATGCTACGGAAG
1321	GATGTTCAATGCTACGGAAG
1322	GACTTGTGAATATCTGTGCC
1323	GCCGCCGAATTATTGAGCAA
1324	TGGACTGATTGATAGGCAAC
1325	
1326	TGGCAGATCGGTGTATTCAA TATGCGTAATGGGTGTTCCA
1327	
1328	TTAGGTCGATTGATAGTCGC
	TCTGCTTTACTGCGTAGCCA
1329	TTGACGAGTTTGCAGTGCTC CTTGATTAAGTGCTGTACGC
1330	CTCGGATCAAGGCTTACCGT
1331	CCGGGCTCAACGCTTTGTAA
1332 1333	TGTCGCCCAGCTCATGTGTT
1334	
1335	CTGGACCACACACATATACC
	CACGGGCCAAGAGATATACC
1336	CGCCGCCAAGTGATGTATA
1337	CGCCAGCCACATGGATAGAT
1338	GCCCGGATACATGCGATTAG
1339	GCTGGCCTACATCCGTATGA
1340	AGATGGCGAAATCCGTATAG
1341	GCAGGGACATTACGATCAGT
1342	AGCAGGTGAAATCGTACTAC
1343	GCAGGTCAATCTCTGTACGA
1344	GCATTGTAAGTTCGGTCAAG
1345	GCACTGGTAATTCAGCTACG
1346	AGCATCATAACCCAAGCTGG
1347	ACCAGTCCAAAGCATAGTCG
1348	ATCATTTCAACGCAGTGACC

Seq. Id	3' to 5' sequence
	<u> </u>
1349 1350	TCAGCCCTATCGCAGGATGT
	GTCAGCACCAGCGTGATTA
1351	GAATTACGCACCCAGCTTGA
1352	GAATGCGCCTACCAGCTATA
1353	GAATGGCGACAGCGTACATA
1354	GGATTGCCACGACTCACAAA
1355	GCTCATTGACACTGCGCTAT
1356	GAGCATGGACCACGGCTATA
1357	CAAATGGACAGACAGCCTGC
1358	CACTTTGAAGCACAATCACG
1359	GCTGTTGCAGGACGCATCTA
1360	TACCTGGCATGACGCGATAT
1361	TTCGTGGACTTGCGGATCTA
1362	TTCCTGCGATAGCGGCGTTT
1363	TTGATCTGATAGCGGGTCTC
1364	TTGATCGCATAGCGTCTGAC
1365	TTCGAGGCATGTGGATCTCC
1366	TTCAGCGGCTAGGCGATTTC
1367	TCCAGCAGATCGGCGAGTTT
1368	TTCAGCCGATCTGCCGATAT
1369	TTCTATCGCATGTCAGCCGT
1370	TGTAATGCCTGCCAGCCGTA
1371	TAATTGCCTGCACAACTGGA
1372	TAATTCCATTGACGGCAGCG
1373	TTATTGCCATAGCGCGACGC
1374	ACAATTTCAAAGCCTGACCG
1375	ACAGGCCCAAAGCACTAGGT
1376	CGAATGCCAAGGCCAGCTAA
1377	GATGGTTCAATGCCTGGACA
1378	CTGGGCCAAGTTCTGAGACA
1379	CGTGGGCAATACAGTTGAAT
1380	GAGCTGCGAATCGGTATTAA
1381	GACCGCCAATCGACCATAA
1382	GACTTCGCAATCGGCACGTA
1383	GACGCGCCAATCGTGCTATA
	GATCGCTGAATCGTGCGTAA
1385	GATCACTGAATGCGACGTAA
1386	GATCGTGCAATGAGGTTACA
	GAGGACTAATTGAGATGCAC
	GACCGATAATTCGATATGCC
	TAGCATTGATCCCATGTCAC
	TTCAGCTTATGCCAGTCGCG
	TGACGGCCTTGCATATCCGA
	GAACGCGCCTTACATCAAGA
	GAATACCAGTTACATCAAGA
	CAAGAACTGTTACACTCCAG
	GACGAGAATGGACTACACGT
1395 1396	TACAGACGCTTGCATAGATC
1330	TACAGACGCTIGGATAGATC

0 1-	OLAS EL SELECTION DE LA CONTRACTION DE LA CONTRA
Seq. Id	3' to 5' sequence
1397	TAACGACCTTAGCGACGGGT
1398	TAACGACGCTTTCCCAAGGA
1399	TTACCGCTGTTGAGCCCGTA
1400	TTCCATGTATCGAGCGTCAG
1401	TATACGCCCTTCAGATCGGG
1402	CTAAGCCTATGCAATATCGC
1403	CCAGCTATAAGCATATTGCC
1404	TACAGCATTGTCATGGACTC
1405	TAAGCTATTGGACATTGGGC
1406	TTAGCATCCTGTCATAGGGC
1407	TCTAGCAGCTTTCATAGCCA
1408	TCATCACGCTTTCCGAGGAT
1409	GCATACATTGGACGAGAGCT
1410	TCTAGCATTTAGCATGGTGC
1411	TTATGACTTGATCTGAGGCG
1412	TGTTCGCACTGGCTTAGCTC
1413	GAGTTGAATGCAGATAGCTC
1414	TGCAGGCTCGCAGATGCTAT
1415	TGCGAGGACTGTAGCTTAAT
1416	TGGGCACTCTCGCCTAGTTT
1417	TGAAGCGCCTCGACTAGGTT
1418	TCATCGGCACTGATAGCTCA
1419	TCATCAGGCATGGAGCCAGT
1420	TAATCAGCGTTACGTCCGCA
1421	GAATGTGACGCAAGTCTGAC
1422	AGATTTGCACAGATAACGCG
1423	GATTACTGACCAGCATCGAG
1424	AACTATCGAAACCGCCAGGG
1425	ATAATACAAGAGTCGCGCCG
1426	ATAATCATAACCTCGACGCG
1427	ATTATCATACAAGGCAGGCG
1428	TATATCGGATCAGCAGGTCA
1429	TAATTTCGCTACGCAGGGAG
1430	TAATCCTGTTACGCGGAGGC
1431	CTTTAGCTCCACGCAGTGTG
1432	TTCTAGCCGTCCGCAGTTTG
1433	GTCATGCGAGCAGCAGTCTT
1434	GGCGTTCGAGCAGTCATCTT
1435	TACCGCCAGTCAGCGAGTTA
1436	TACCGCCTAGCAGCATTGGT
1437	TACCGCACTGCATGTCAGGT
1438	TGTCTCGATGCAGGTCTAGT
1439	GCCGCATGACGAGGATATAC
1440	TACCGCGAGGCAGGATTCTT
1441	TACAGCAGTGCAGGGCCTTA
1442	GCAGCTAGAGCAGAGTATCA
1443	GACAGCAGATCAGAGACTCC
1444	TAAGCACGTTTAGAGCTGAC
	INGONOGITIAGAGOTGAG

Seq. Id	3' to 5' sequence
1445	TAACCGTGTGCAGATCGGAT
1446	TACTGCGGACCTGGATCTAC
1447	TCAGGGCTACTCGATTGGAA
1448	TCCGCAGACTTAGCGTTACG
1449	TGAGCAGCCTACGTTACTAG
1450	TGCGTCAGATGCGTATATGC
1451	TCGTCCAGATGCGGAGTTCA
1452	TCGGCTATATGCCAGATCCT
1453	AAGGACAAAGAGCGCGTCTC
1454	TAGCACCGATGGCGAGCTTA
1455	TGTCCACGGTGCCGCAATAT
1456	TGGTCCGACTGCTGCTACTA
1457	TGTGCCGACTGCCGTCTTAT
1458	TTCGCAGTATGGATCGGTAT
1459	TTACGCAGTTGCATGGAGCT
1460	TTCTGATTAGCTGCGGACGC
1461	TGGTTATACTTTGCGAGAGC
1462	TTTGTTAGCTTCGGGCAGCC
1463	TTGGTCTGATCCGGGCATAC
1464	TGCTTGGACTCCGGCGATTA
1465	CTGCTTGGACCAGCCAGTTA
1466	AAGCTGGGAAACGCACACCT
1467	AAGCGGGCAAACGATATGCT
1468	AAATGCCGAAACCATCTCGT
1469	CCATTCGGAAGCGACTCGAT
1470	TACATGGGCTGAGAACGCAA
1471	TATTGGGCACGAGCGCCTAT
1472	CATCCGGGAAGAGTAGCACA
1473	ATTTCATGCACATAGCACGC
1474	ATTGCAGCACAAGCCAGACT
1475	TTGCTAGGCTCAGTCCCGAT
1476	TTGGCGAGCTGCGTTCTCAT
1477	TCCCAGAGATGCGACTGCTA
1478	TTCGCTGGATCGGCATGTCT
1479	TTGCTCCTAGCTCGCGTGAT
1480	TTGCTGCTAGTCCAGTAGGC
1481	CATTAAGCAGTCGAGAGACC
1482	CGTTAATGCAGCGAGAATCA
1483	CGCAAGCTCAGCAGAATTAC
1484	CCATGTCGAAGCATTCATAC
1485	CTGAATGTAATCATCGTGCC
1486	CTTAGATGAATCACTGCCAC
1487	CTTCACGGAATCTAGGCACA
1488	CACTCTTGAAGCTAAGCACA
1489	CCTCTAAGCATGTTGACACA
1490	CATGCCGGAAGATGCGTACA
1 491	CAGGCAGCAAGATGTACGAC
1492	CAGTGGGCAAGATAAGATTC
1-7-7-2	DAGTAGGATA

Coa ld	2' to E' coguence
Seq. ld 1493	3' to 5' sequence
	CCGTGCCCAAGCTAGTGATA
1494	GATCGGGCAATCTGCGTACT
1495	TTCAGTGCATTATAGTGCGG
1496	TTATCTGCATGAGTAGGTCG
1497	TCGATAATCTTTGTAGCGCG
1498	TCTTACAGCTTTGCAGGGAG
1499	TCCTACATTTGCCACGGGAG
1500	TCTTCATCAGTGAGGCGCGA
1501	TTTCTAGGATGTATGCGAGC
1502	TATCCAGCATTACTGCGAGA
1503	TTATTCTCAGCACGCACGGA
1504	TGATTCGCACTCGCGGCTAA
1505	TTTGTATGAGTCGCTCCGAA
1506	TTCCGATCAGTCGATGCAAA
1507	GATCGTCAATCTGATGCACC
1508	AGATCGCTAAATGAGGACCC
1509	GATGCTATAATCGTATGGCC
1510	AGGAGCGTAAATTATCAGCC
1511	GGGCGATGACTATATCTGAA
1512	CTGGATTGACACTAGCATAC
1513	CTGCGGATACCATAGACAAC
1514	ACTGCAATAACATATCCGCG
1515	AATGACATAAAGTGCTGCCC
1516	ACATGCAGAAAGTAGTCCGC
1517	ACAGGCGAACAATGTACCCG
1518	ACCAGCACAAAGTCTACTGT
1519	AGAGAGCCAAATGACTGTCC
1520	TAGTGCATAATTGCTTGCCC
1521	TGAGCATATAGTATTCGGGC
1522	TGAGCGTTAGAGCTTGATCC
1523	TAGGCGCTAGGACTCGTTAT
1524	TATGGCCGACGATGTGTCAC
1525	TATGGCTGACGTAGCGCACT
1526	TCTCGGTTACTGAGTGGACT
1527	ATAACGGGACAGAAGCTGCT
1528	ATAGAACTCAATAGCCGCTC
1529	CATAATACACATACGCTGCG
1530	CAGTACGCAAGCAGATAGCC
1531	CAGACGCGAAGATAAGTTCC
1532	CAGCCAAGATAGCATACTCG
1533	TCCCATAGATAGCTCGCTGG
1534	TTCGCATGAGTGCTGAGTAC
1535	TTCCATATACTGGTCGGCAG
1536	TTTATGATATGCGTCGCGGA
1537	TTTCTTATATGCGCGAGCGG
1538	TGTTGCATATTAGCGGCTCG
1539	TATATGACATCTCTTGCCCG
1540	TTGTCACATTTGCGCTCCGA

Seq. Id	3' to 5' sequence
1541	GCATCCGAATTGCGACGACT
1542	GGATCTGAATTGCGCGACCA
1543	GGCTATGAATTTCGCATCAC
1544	GGATATGCAATTTGTAGCCC
1545	CAGCGTATAGCAAGATGGAT
1546	CGAGCGATAATCAAGTCGAG
1547	CGCGGATGACACATACTCAG
1548	CGACGAGCACCAATTCGAGA
1549	CCGTAGTGACCAATGCAGAC
1550	GCGATATACATCATTCGGAC
1551	GACAGTCTAATCACTCGTAC
1552	GCAGTTATACTAAGGTGTGC
1553	GCAGTAGTAATGAGTGTCAC
1554	GCAATGTAGTCGAAGTGTCT
1555	GCATATAGATACCATTCGCG
1556	CGAATACTAGACACATTGCG
1557	CAACTACAGTACACAGCGTG
1558	AGACACAGAACTACCGCGTG
1559	ATAGCACAACGTAGACGCCG
1560	ATACAGTCAACTACATCGCG
1561	AGTACAACCTAGAATCCGGC
1562	GAAGACTACTAGATACGCGC
1563	CGATAATACTACAGACTCCG
1564	CCGTGCGTACACATAGATCA
1565	CGTGAGCGACACATGATCCT
1566	CTGTAGTGACATATAGAGCG
1567	ATGTCGTCACACAGAATACG
1568	ATGCTACGAACTACCAATCG
1569	ATGATACGTACACACCTGC
1570	TCGGTCTACGTCTGCTCAGT
1571	GGCTCACGATCCACTGGTTA
1572	TGCCTGATACCTTGGATGAC
1573	GGCCGTGATTATCATAGAC
1574	GGCTTGGACTTATCATAGAC
1574	CCCATCGAAGCATGTAAAC
1576	CGGCATCGAAGGCGTTCATA
1577	GCCAGTTGACCACTTCTGAG
1578	TCGCATTAGCCATGTGGAGC
1579	GCAATCTAGTCTAATGGCGC
1580	CTAAGATGTTCTAATCGCCC
1581	CCAATAGTAAGTAATGGGCC
1582	TCATTATACTCTGATGGCCC
	ATGCTAATAACTGATCGCCC
1584	AGTGTCAACCATGATGAACC
1585	AGAGCATAACATCATGGCCC
1586	AGAATCTAACAGCGATGCCG
1587	ATTTAGACAAGTCGATGGCC
1588	ATATTAAGAAGTAGGCGGCC

	<u></u>
Seq. Id	3' to 5' sequence
1589	CATATCAGAATACGATGGCC
1590	GATATACAGGATTATGGCGC
1591	CATAAATTGGTTCACACCGC
1592	GAAACTCCAATTCAGCGGAC
1593	GAACAATGAATTTAGCGGCC
1594	TTCCATTAGATGTGATGCCC
1595	TATCATATCATCTGAGGCCC
1596	ATCAGAAGAACTGCACGTCC
1597	AGCACAAGAACTACGCGCTG
1598	AGCAAAGAACCATGCCGCGT
1599	TAAAGAGCAATGTGGCGTAC
1600	TTCAGGGCATTGAGCGTAAA
1601	TTAATGGGCTTGAGCGTATC
1602	TTAATGCGGTTGAGATCGAC
1603	GCAGGGATAGCAGATACATC
1604	TCAGGAGAGGCATCGCATCA
1605	TTATCTTAGGGATGCGGATC
1606	TGTGCTCTAGGTCATCCGAG
1607	TTGTATCTAGTGCGAGGCAA
1608	TATTATCTAGTATGCGCGGC
1609	TAGTTATCAGAGTGACTGCG
1610	GTTAGATCATAGTCACCGCG
1611	GTTAGTATAGATTGGCCGAC
1612	GTGTTTATACGTTGAGCACG
1613	TTATCTGTAGTCATCGAGGC
1614	TGATACTGAGTTAGCGAGCT
1615	GTGATCTCAGAGCGCAGCTT
1616	CAGATGTCAAGACGCGGACT
1617	CTGGTCAGACAGCGGAATCT
1618	CGTGGCAGACAGCTAGATAT
1619	GTGCCGAGACTCCACTGTTA
1620	GCGGACAGCTCTCCTAGTAT
1621	ATGCACAACTATCAAGCCTG
1622	GTGCTTTACTAGCGGAGCCA
1623	TAAATATCGTATAGGCGGCG
1624	TAATTCTACTATACGCGGGC
1625	TAAATCGTATGTAGCAGCGC
1626	TCCTTCACTGTAGGCTAGGC
1627	TCAGTTATATGAGCCGACTC
1628	TCACGTATATTGACTCCGAC
1629	TCACCGTATTCGAGGCGACA
1630	TCGTACTGATTGACGGTGAT
1631	TCACAGCGGTCGAGGTTACT
1632	TTCACGCGGTCGCAGTATCT
1633	TACTTGACGTGACTGCATCG
1634	CGTCACAGAGGACAGCATAC
1635	TCACTAGAGCGTCGAGCTGT
1636	TCTACAGTGTGTCAGAGTGA

Seq. Id	3' to 5' sequence
1637	CTACCTAATCGACAGCAGAG
1638	CACCGATAACTACAGCAGGG
1639	CAACGTCTAGGACAAGGCAG
1640	CACTAGCTCAGACAGACGAG
1641	GACTTTACAGTACGATCAGC
1642	GACACTGACTGACATCGAGA
1643	GAGACAGTCGAGCGATCAAT
1644	GCACTTGTACGTCCAGTCAG
1645	GTACACGGACTGCCAGCATA
1646	GTAATACGCTATCAGCAGAC
1647	CTAGATAGACATCACTCACG
1648	TAGACTCTCGATCAGCCGTA
1649	GACTTGCACGTACAGCCGAA
1650	CTTATGCGACACTAGCTCGA
165 1	CTGATGCTACACTAGGCACA
1652	GCAGACGCACTATCATATAC
1653	GCAGTAGACACTTCTCACGA
1654	GCAGGTACACTGACCGACTA
1655	GCACATCACTGCACGATAGA
1656	GCAATGACTTCGACTCCAGA
1657	GACAAGTCATTTACAGGCGA
1658	GTAACTTGTTTGACAGTGCG
1659	GACACTGCATGGACAGCGTA
1660	GCAAGGACTGAGACATGCTT
166 1	TGCGAGGTAGGTTATATCTC
1662	TGCGGAGAGTGATATACTTC
1663	GGCGTGAGAGCATTATATCT
1664	GTGCTGCGAGAGTATTATCT
1665	CCGCGTGTACCATATAATAC
1666	GAGCGTGGACGATATACACT
1667	GGCCGTGTACGATTATGACT
1668	GTAGCTTGACGATGCTGACT
1669	GTGCTGGTACTAGCTGCTCT
1670	TAATGTGACGTAGCCGACTC
167 1	TACCGAGTGCGAGATGCTCA
1672	TACCGATGTCGATAGATCCA
1673	TCTCGTATAGGATGAGCAAC
1674	TCGTGAGTAGGATGCTTTCA
1675	TACGTGAGATGATCGCT
1676	TAGTCGGTAGCATGAGTCTA
1677	TAGTTCGAGGAGTAGTCATC
1678	TAGGTACAGTGCTGGATACT
1679	CTGCGTCAAGTGTGTAGAAT
1680	TGTGCGCTAGAGTCTGTCCT
16 81	GGTGCGTCACGATCTCCTAT
1682	GTGTGGGTACTATGCCATCA
1683	GCTGATGTACTATCCATACC
1684	GCTAGATGACGATCAGGTAC

[Com Id	O'to E' comune
Seq. Id	3' to 5' sequence
1685	GCATCTGTACGATCTCAGCA
1686	GCATCACGACGATTATCAGA
1687	GCTACGTTACCATGTGCAGA
1688	GCGTAGTTACCATGCTCACA
1689	GCGTGAGCACACTCTATCAG
1690	GCGTGCGAATTATGTATCAG
1691	TGTGGACACTTCTTATAGGC
1692	GCGTGAGTAATTTGACTACG
1693	AGGTGCGTACAAATGCTATG
1694	CGCAGCCGAAGTACGCTATA
1695	CGACTGCTAAGGAGCGTACA
1696	CGATGTTGACAGACCGCACT
1697	CATGTAGAACTGACTCACAC
1698	CGAGCGGTAAGGATCTCACA
1699	ACACGCTGAAAGAGTACGCC
1700	GATCTGACAGGTAGCGATAC
1701	TCTCGTGCAGGTAGCTGTCA
1702	GCTCGGACAGATCGGTATCA
1703	GCCGGTATAGCTCGATATGC
1704	GCTGATACAGTTCGATAGAC
1705	CCTGACTAAGCTCGATAGAG
1706	GCTGATTACGATCTAGTAGC
1707	GAATGCTCACGACGAGTAGC
1708	GAACTGTCCTGACGAATGAG
1709	TTACTGTCTATGCGATCCGA
1710	GTTATGTCATCGCAGATTCC
1711	AGCTATATCAAGCAAGCGTC
1712	GCTTATACAGTGCAGTAGAG
1713	TTAAGTAGGTAGCTGGCCTC
1714	CAAGAGTAACTGCAAGGCCC
1715	CACTAAGACATGCACAGCGG
1716	CCTAGTGCAGACCACATGAT
1717	TCATGCACGTCGCCATAGGT
1718	TCTATACGCTCGTGCAAGGA
1719	TCAAGCCCGAGCCGAGTTTA
1720	TCAGCGCCAGCATTCATGGT
1721	CCATGCGGACCAAGTCGATA
1722	GAATGCCGAGCAATGATCCT
1723	GAATCGGCAGCAATACTGTC
1724	GAAGCCCAGCTAAGTGGTAT
1725	AACAGCCCAAACCGGATGGT
1726	TAAGCACCTTGCAGGATAGA
1727	TCAGCCCGATCCAGGGTATT
1728	TATGCGCCCAGGAGGCTTTA
1729	TGCCCAGCAGGTCGGATTAT
1730	TAGCTCGCATCACTGACGGA
1731	GGTCCCATACGAGTGGCATA
1732	ACTACCCAACAGCGGAGGT
1702	PIO I ANDOUANDA I

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Seq. Id	3' to 5' sequence
1733	CAGCTCTAAGCAGCACAGGA
1734	CAGGTCAAGCACATACCAGT
1735	CTGTGCAATCACGCCAGAGA
1736	CGGCGCAATAATGTCACAGA
1737	CGGGACATAATTGACACAGT
1738	AGGGCCAGACAATACACCGT
1739	GAGGTCACAATTTGCTACAC
1740	CAGGCACAAGATTGAGCACG
1741	ACAAGCGCAAATACTGCCGG
1742	ACAATCTGAAATAGCGCGGC
1743	ATCGACCCAAGAATAGCTCG
1744	ATAAGCACAAGCAGCGCGGT
1745	AACACTCCAAACCGAGGGTG
1746	AATCTATCAAAGCGACGGCC
1747	ATTCCCATAACGCGGAGGAC
1748	ATGCCAGCAACGCGCTAGAA
1749	ATGCTCACAAGCCACGAGAG
1750	ATGCTCCAACGATACATACG
1751	CAGCTTCAAGAGTACATACG
1752	CATGTCACAAGGGCATAGAC
1753	CATGGTCTAAGCCCTACAGA
1754	ACATGGCGAAAGCACCACGT
1755	CTTAGTTCAATGCACGCACG
1756	CGCCAGTTAATGCACGACAG
1757	CAGCAGCAACTCGACTAGAG
1758	CCGAAGTCAACTGCGCTAGA
1759	CCAGTGTCAATAAGAGACGT
1760	CCAGGCGAACTGATCGTAAA
1761	CCTGGTACAATCAGTAGCAA
1762	CTAGTGGCAATCATCAGACA
1763	CAATGCGAACTCACTAGACG
1764	CATGGCGTACCAATACCTAG
1765	AAGTGGCCCAAATAACTGCC
1766	CAAGGCCCAATACACAGGGT
1767	GATCTGCCAATGCCGCGATA
1768	GATTCGCCAATGTGCGCTAA
1769	GAGCCGCCAATGTCACTAGA
1770	GCGCCGGAATGTCGTATAT
1771	GCCGCGCCAATGTTACGTTA
1772	CTTCGCCCAATGCGTAGGAA
1773	TTCCCATGATCGCTGACGAG
1774	TTGCGGGAGCTGCCTCTTAA
1775	TTTCCCGGATAGCCGCTGTA
1776	TTTGCTGGAGTATGCGCTCA
1777	TTGTTCTCAGCTTGCGGCAG
1778	TGTGTGGCAGCTTAGTTCAC
1779	TCTTGGGTAGCATCTACCCA
1780	TGGGTGTCAGCATCTACGCA

Con Id	O' to E' approprie
Seq. Id	3' to 5' sequence
1781	TTGTGGCAGGTATGCTCCAA
1782	GTTGGGCACGGATCTCTATA
1783	GCCGAGGCACCATGCTTATA
1784	CGCTTGGGACAATCGCGTAT
1785	CCGCAGGGAACTTCAGCATA
1786	TGGAGGCAGTCTCTCATAA
1787	CTGGGTGCAAGTTGTATCAA
1788	TGGCGCACATGGTGTCATAA
1789	TGGCATCACTGCTGCGGAAT
1790	TGCCAGTCATCCTAGCGTGT
1791	TCAGGCCAGGACTGCTTATC
1792	TTGGCATAGGAGTGCTTCTA
1793	TTTGCAGACGGTGTGCTATA
1794	TTGAGTCAGGGTGCCCAACT
1795	TTAATATCGTTGCCCGAGC
1796	TCAGGATGATGAGCATGTAC
1797	CTCAAGCTGGGAGAACAGTA
1798	TCAGAAGTGGCTGGATCATA
1799	TCTCACATGGCTGGAGCATT
1800	CTACTGACACTGACCAGGGA
1801	TCGTAGCGACTCTCCAGGTT
1802	TACGTGTCACTATCGTCGAG
1803	TATAGTTACGTCTCGCACGC
1804	TACCGTTACGTCGCTCAGAG
1805	CACTACAACGTGCTACAGAG
1806	ATAGGTATAACGCAGTACGC
1807	ATAGCAGTAACGCATAGTCC
1808	ATAATCGTAACGCACCGACG
1809	ATGAGTGTAACGCCTCGACA
1810	ATGTAGCGAACGTACTCACA
1811	ATCTAGCGAACGGAACTATC
1812	GTAGAGTCACGATGCAGTAC
1813	GTAGTATGACGTAGCAGTAC
1814	GTACGTCGAGCTAGATCGCT
1815	GAGTCTGTACGAGGTATCAT
1816	CGTGTCTTACAGCACTACAT
1817	CGTGCGCTACAGCAGTCATT
1818	GTAGCCTAGACGCAGTCGTA
1819	CGTCTCGCAAGTCGCGTATA
1820	AGTCGCGCACAGCAACGTAT
1821	ATCGAGGTAACGCCATATAC
1822	CTCGTGACATAGCCATAGAT
1823	ATGCGACGAACGCGGATATA
1824	CTAGACAGACTGCGACATAC
1825	TAGTCGTAGAGGCGCTATCA
1826	CTATCGAAGTCGCGTGAAAC
1827	CTGCGTATAGAGATCAATCC
1828	CCGCGTATAGACAGATATGA

3' to 5' sequence
CTCGCTTACGACAGACTGGA
CGCGCACGAGACAGACTA
AGCGTCACACACAGACTGG
CCTACGAGACACATGACAGG
· · · · · · · · · · · · · · · · · · ·
CGCCGAGTACACATGCAGAT
CCGTCGATACAGACTCAGAT
CTCGTCAGACAGAGCGGATT
GTCTCGCCACGTATCGGATT
TCTCGCGTACTTAGGCATCA
GTCTCGGTACGATGTAGCAA
CGTGTGAGACAGTAGCATAT
CGTGTAGCACAGCGACGATT
GTGTAGCTCAGTCAGCATCA
AGGTAGATAACGCTAGATCC
CTGTAGAGACATCTGAATCC
CTGATACGAAGTCTTATGCC
CACGCTCGAAGACTAATGAC
CACGCGATAAGACGTATAGC
CTAGCAGTAAGTCTATGCAC
CGTAGTTGAAGTCATCGACA
CGCGATAGAAGTCAGGACAT
GACGGACGACATCTGAGCAT
CATAGACGAATACAGCGGGC
GATCACGACCTACTAGCAGG
AGATATAACGAACTCTCGCG
GATTATAGACTACTGAGGCC
GAGTTTATACTACAGTGCCG
GTCACTTACGCTCAGGCAGA
TCGCTAGACGCTCTGGCATA
GTACGCTCAGCACTGGCATT
GACGCGCTAATACTGTCACA
GCGTGCATACGACTGCCATA
TGTAGTCTAGTGCATGGTCA
GTATAGTCAGAGCTGGCACC
CGTCAGTCAAGTATGGCACA
ACGAGAGTAAATATGCTGCC
ATAGAGCGAACGATAGTTGC
ATCTGACTAACGATGATGCC
GTTGTAGGACGTATGATCTC
TTAGTCGAGTCTATGAGCCC
CGACGATACAGTAATCTAGC
CTGATACAGGCATAGACATC
GGTATCAGAGCTAGGACTAT
TCTATCTCAGCTACGGTCGA
TCAGTTCGATCTACGGCTAG
TCAGTGCGACTCAGGTACGA
GTCACTGCACTCACGGTAGA
TAACGAGTCTTCAGCACGTA

Seq. Id	3' to 5' sequence
1877	GAAGTCGCCTACATAGCCTA
1878	GAAGTCCGTTACATGACCAT
1879	GTCAGAGGATCGAGCCACTT
1880	GCGAGACAGGTCAGTACAAT
1881	CGTCAGAAGGCTCGCACATA
1882	GCATACAGGTTACGACGCCT
1883	GCGATACAGGTTCAGAGATA
1884	GGACGCATAGCTCGCAGTAT
1885	GGACGCAGATCGCAGCATAT
1886	CGGCGTTAATCGCAGAGAAC
1887	CGCGTTCTAAGGCACGGATA
1888	CGCGTCGCAAGGCTGTTATA
1889	CGATACGCAAGGCTACGACA
1890	CATCTAAGGACACTACACTG
1891	TATCATCGAGGACTCAGTGC
1892	CACCGAGCAAGACTGACATG
1893	CGCACCCGAAGTCAGAGATA
1894	CGGCTAGGAAGTCAGCATAA
1895	ATGCTGCGAACGCGCCATAA
1896	CCGCGTGCAACGTGTTCATA
1897	GTCGCTGCATAGCATCTCAG
1898	GTCTGTGCATAGAGCGTCAT
1899	GTGGTGTCACTGATACGTCA
1900	GGTTAGCACTAGATCGCACT
1901	CGGGATCTACAGCATCATAG
1902	CTGGATATACAGCACTCACA
1903	ATGCGGCTAACGCCTCATAA
1904	TCGCGGCGCACTCTGTTATA
1905	TCGTGCTACTGCCACTGTAT
	TAGGACACTTCGCCACTATG
1907	TATGACAGTTCGCGCTACCG
1908	TCGCGCAGTTAGCCCTATGT
1909	TAGCCACCGTAGCTGATCGT
1910	GTAACCCGCTATCAGATCGA
1911	AGAGCGCAACACCACATTGT
1912	AGGCTAAGAACGCACACTCG
	GAGCCTAGACAGCTTCATAC
	GGCAGTTCACGACTCGACAT
	GGCCTTAGACGACTCGCATA
	GGTCGATCAGCACTGCATAC
	GGAGAGTCAGCACAGTCCTA
	GTATAGGCAGCACGGCTCAT
	GCACGGCGAGCACTATCTTA
	TAACGTCCTGCACGATCTGT
	GGACGCCTAGCACATCTGAT
	CGCTGCACATCACATGGATT
	GCACATCGAGCACATGCAGT
1924	GCACGACCAGCTCTTAGGAT

C-~ 14	10/40 F/ 00000000
Seq. Id	3' to 5' sequence
1925	CCCACCAGACAGATAGAGGT
1926	CCCGACGCACGAATAGATAG
1927	CCCACGACAGATACATGAGT
1928	CTTCGCGCAGCTACATAGAT
1929	CGCTCCGAAGCTGCGATAAT
1930	CGCCGCGTAAGCAACAAATT
1931	CGACGCTCAAGGACTCATAA
1932	CGCACACTAAGGATCATTAC
1933	AGACACGCAAGAAGCTGGCT
1934	GCACGCATAGCAGAGGATCT
1935	GCTACGTCACTGAGCAGGAT
1936	GTACATCTCGTGAGCAGAGC
1937	CTACACGACTTGAGACGAAG
1938	CTAAGTACGTGCAAGCAAGG
1939	GACACGTAGGACAGCTATGC
1940	GACATAGTAGACATCTCACG
1941	GACAGCGTAGACATCGTCAG
1942	GACTATCACGACATTCAGCG
1943	GATCTACACGCTACCAGTGG
1944	GCTTACTACGGATAGATCAG
1945	GCGTATCTAATGGAGTAGCA
1946	GCGTATTTACAGTGAGCGAC
1947	GCGTATATCGAATTGAGTGC
1948	GCGTTCACAGAGTCCACGAT
1949	CGCGTATCAAGGTCACGACA
1950	GCTATTACAGTGTCAGAGAC
1951	CGTCAGATAAGGTGAGTTAC
1952	CGTCTGTGAAGGTCAGCTAA
1953	TATTAGCACTCGTCAGCAGC
1954	ATGTTATCAACGTCAGCGAC
1955	GGCATACTAGAGTCAGCGAT
1956	AGTGCGATACAATACGAGCG
1957	CAGCACAGAGTACAGCGT
1958	CGTAGCATAAGGTCAGCACC
1959	GTCCATAGACGTTGATACCA
1960	GCTACGATAGATGAGCCACG
1961	CGGAGTACACCAGATCCAGA
1962	GAGCGTATAGGAGATCCAAC
1963	GACTGTAGAGAGACGATCCA
1964	CTAGTAGGAAGTGCGATCAA
1965	CGTAGAGGAAGTGATACTCA
1966	CGTATCGGAAGTGAGTATCA
1967	CTATGACGAAGTGAGAGTAC
1968	GTTCGTAGAGATGATCGTCA
1969	GTTCTCAGATAGTATGCAGC
1970	AGTCTGTTAAGATATGCGCC
1971	AGCACGGAACAGTAAGCCCT
1972	ATCCAGAGAACGTGAGATCC
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Seq. Id	3' to 5' sequence
1973	GACAGTGTAATATGAGGACC
1974	CATAGTAGAAGATTCGAGCC
1975	TGAGATATAGTATGCGGCCA
1976	ATGAACATACTATACCGCGC
1977	TTCTCTATATCGTGCGCGGA
1978	TGAGTTTACGTGTATGGCAC
1979	ACGGCATCAAAGTTGCATAC
1980	ACGGGCTCAAAGTATGATAG
1981	AGGCGCTTAAATGTGGATAC
1982	CTGCCGTTAATGGCGGACAT
1983	CTGAGCCAATAGGCGCACTT
1984	TAGGCATGATGAGAGCTATC
1985	TGCCTATGAGGAGTATGAAC
1986	GGGCTATAATGAGCTTGACT
1987	TAGGCTTCATCAGCTATCAG
1988	ATTGCTTCAACGGGCATTAC
1989	TATGATCCATGCGACTCGGA
1990	TTGTATCCATCGGCCCAGTG
1991	ATCAAGGCAACCGCCAGTAG
1992	TCTCAGCCATCCGTGATAGG
1993	TATCAGGCATCCGAGCATAG
1994	TTAAGCTCCTCAGTCCATGT
1995	TAAGGGCGATGAGCCTATCT
1996	TAAGGCCGAGGAGCTTTCAT
1997	TAAGGCAGTGGAGCCCTCTA
1998	TGGACAGGCTGCGCTCTATA
1999	CTGGAAGCCTGCGACCAAAT
2000	TCAATGCACTGAGCCCGAGA
2001	GATTCACACTGACCCATGTA
2002	TAAATAGATTGGAGACGCGC
2003	GCATTAGAAGGTCTGGACTA
2004	ATTGGCATAACGTATTGCGC
2005	CAGGACTGAAGATCGAGTAC
2006	TAGAGTCAGTCATAGCTCGA
2007	TTTATCGTAGCTGGCTGCCC
2008	AGGATTAGAACCTACGCACC
2009	GCCGTGAGACCACTGTACTA
2010	GACGCTGAATCCTATTGACA
2011	CGCCTAAGGATCGTGAAGTA
2012	CGACGACGAAGCTGCATGAA
2013	ACTCGAATAACAGCATCTCG
2014 2015	CCCGTAAGCATGGCACAGAT
	CATACAAGATTACGGCCTC
2016	GATCAGAATCTATGGTACGC
2017	TCTGTGTACTGCTCGCCAAT
2018	ATATTTGGAACGCAGCTCAC
2019	TGCAGTATCGCAGGCGGTTCTA
2020	GGGCAATGTTTATCCACAGA
2021	CTGACCGAATCCAGCAGAGA

Seq. Id	3' to 5' sequence
2022	GATCGTGAATCCGCGCACTA
2023	GAGCCGTAATCCGAGCGATA
2024	TACTCCTGACGACTTAGGCA
2025	TGCTGTCACTCGGCGTCTAT
2026	GTACTAGCATATCATCGACG
2027	TATCGCATAGATCAGTGAGC
2028	TACGGGCAGCCAGGTACTTT
2029	GTTCATCACGAGTGCGTAGA
2030	CATGTATCAAGATGGCTGAC
2031	GGTCGCGCATTCCAGCATA
2032	GCACATATCTAGCGACATCT
2033	ACGCGGCTAAAGGTAGATAC
2034	CACTGCCCACAAGATGTAGA
2035	GGATTTACATGGCCTAGCAA
2036	CATGACACAGAATCGACCGT
2037	AGAGGCATAAATGAGTCTCC
2038	TGAGTAGTACGTTACGCCTG
2039	CGATAGCGAAGGAGTCCACA
2040	ACACTCTGAAAGACGCGACG
2041	GTCTTAATGTTGGGCAACG
2042	GTTATCGACTACGCTGTACT
2043	TCGTGAGACCGTCGTCAGTA
2044	GACAGCGCAGTACAGGTAAT
2045	CGTACAGTAAGTATGATGCC
2046	TAGAGCATCTGACGCTATGA
2047	GTCACGATTAGTAGGCACG
2048	TCGTACCTGTATTCAGCGCG
2049	TTAATCCGCTGTAGCCCAAA
2050	TTAATTGACTTCGCTCCAGC

EXPERIMENTS

Arrays containing probes corresponding to SEQ ID NOS 1-2050 were designed and manufactured using known photolithography techniques. Four probes were designed to interrogate each sequence from SEQ ID NOS 1-2050: a probe designed to be the perfect match complement to the sequence (PM), a probe designed to have a central mismatch at position 10 (MM), and probes designed to be the complements to the PM and MM probes (cPM and cMM respectively).

FIG. 2 shows an example of the sequences attached to each of the four array features representing a given tag sequence. The first block contains the cPM probe. The second block contains the cMM probe. The third block contains the PM probe - the probe to which the tag is expected to hybridize with the highest affinity. The fourth block contains the MM probe.

- FIG. 3 shows the array features from the above-described array. The array was hybridized with biotin-labeled oligonucleotide tags, stained with streptavidin-phycoerythrin, and the data was collected with a laser scanner. Four features, organized vertically on the probe array, represent each tag-probe. For each of the four tag-probes shown, arranged horizontally across the array, the brightest hybridization signal is seen with the "PM" feature.
- FIG. 4 is a scanned image of the hybridization pattern resulting from the hybridization of 2050 different oligonucleotide tags labeled with phycoerythrin to an array designed as described above.
- FIG. 5 is a scanned image of the hybridization pattern resulting from the hybridization of 50 sequences complementary to SEQ ID Nos. 2001-2050 to an array designed as described above.
- FIG. 6 shows signal intensities from two different independent experiments in which 2000 biotinylated oligonucleotide tags or 50 fluorescein labeled control oligonucleotides were hybridized to arrays designed as described above. The frequency of results are shown as normalized (to scale of 0-1, in bins of 0.05) natural logarithms of the net signal intensities. The normalized natural logarithm of the signal intensities obtained are distributed about a geometric mean of 0.8 with a standard deviation of less than 0.1.
- FIG. 7 shows the PM/MM ratios from the data described in FIG. 4 above. More than 98% of the hybridization's yielded a PM/MM ratio greater than 3/1.

CONCLUSION

The above descriptions are illustrative and not restrictive. Many variations of the invention will become apparent to those of skill in the art upon review of this disclosure. The scope of the invention should, therefore, be determined not with reference to the above description, but instead should be determined with reference to the appended claims along with their full scope of equivalents.